

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 19:02:13 ; Search time 9258.62 Seconds
(without alignments)
3097.698 Million cell updates/sec

Title: US-09-827-854A-2

Perfect score: 1493

Sequence: 1 KVEQAVETEPELROQTEW.....VEKQAAVGTSAAPVPSDNH 299

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -HOST=LOCAL
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_pat.*
3: gb_ph.*
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13: gb_in.*
14: gb_cm.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1493	100.0	1110 2 E00359	E00359 cDNA coding
2	1493	100.0	1110 2 E00823	E00823 DNA sequenc
3	1493	100.0	1147 2 AX302545	AX302545 Sequence

ALIGNMENTS

RESULT 1

E00359

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

E00359 1110 bp RNA linear PAT 29-SEP-1997
cDNA coding human apolipoprotein E3.
E00359
E00359.1 GI:2168646
JP 1985118189-A/1.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1110)
Teranishi,Y., Takamatsu,N., Matsui,Y., Kimura,M. and Ikeda,Y.
DNA FRAGMENT
Patent: JP 1985118189-A 1 25-JUN-1985;
MITSUBISHI CHEM IND LTD
OS human
PN JP 1985118189-A/1
PD 25-JUN-1985
PF 29-NOV-1983 JP 1983224980
PI TERANISHI YUTAKA, TAKAMATSU NOBUHIKO, MATSUI YASUSHI, PI
KIMURA MASAKO,
PI IKEDA YASUKO
PC C12N15/00,C07H21/04//C12P21/00;
CC strandedness: Double;
CC topology: Linear;

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C0785970 Sequence
C0875269 Sequence
C0896276 Sequence
C0963896 Sequence
C0981476 Sequence
DD166083 Treatment
AR380462 Sequence
AX821568 Sequence
X00396 Homo sapien
BC003557 Homo sapi
AR531680 Sequence
BC072022 Homo sapi
E08423 DNA coding
BD004277 Apo E hum
DD166085 Treatment
I15975 Sequence 1
AX333278 Sequence
AX409597 Sequence
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BD004279 Apo E hum
CQ719877 Sequence
BD084811 Diagnosi
AF261279 Homo sapi
AX358722 Sequence
AF050154 Homo sapi
AC011481 Homo sapi
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DD166084 Treatment
MI0065 Human apoli
AF261280 Pan trogl
AC146473 Hylobates
AC145523 Papio ham
AC151887 Saimiri b
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AF200502 Gorilla g

CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue_type=liver;
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FT mat_peptide 69..965
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/mol_type="genomic RNA"
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FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 1.04e-120 Length: 1110
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-827-854A-2 (1-299) x E00359 (1-1110)

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QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTrpVal 40
DB 129 CAGAGCGCGCAGCGCTGGGAACCTGGCACTGGTTCCTTTTGGATTACCTGGCTGGTG 188
QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
DB 189 CAGACACTGCTCAGCAGGTCAGGAGGAGCTCTCAGCTCCAGCTCCAGGAACTG 248
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTrpLysSerGluLeuGlu 80
DB 249 AGGGCGCTGATGACGAGACCATGAAGAGTTGAAGGCTTACAAATCGGAATCGGAGGA 308
QY 81 GlnLeuThrProValAlaGluThrArgAlaArgLeuSerLysGluLeuGlnAla 100
DB 309 CAACCTGACCCCGTGGCGAGGAGACCGGGCAGCGCTGTCCAGAGGAGCTGCAGGCGCG 368
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTrpArgGly 120
DB 369 CAGGCGCGGCTGGCGCGGACATGGAGACGTGTGCGCGCGCTGGTGCAGTACCGCGCGC 428
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluLeuLeuArgValArgLeuAlaSerHis 140
DB 429 GAGGTGAGGCCATGCTCGGCCAGAGACCGAGAGCTGGGGTGGCGCTCGCGCTCCAC 488
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
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QY 161 ValTyrGlnAlaGlyAlaArgGluGlyValaGluArgGlyLeuSerAlaLeuArgGluArg 180
DB 549 GTGTACAGCGCGGGCGCGAGGGCGCGAGCGCGCTCAGCGCATCCCGAGCGCGC 608
QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyValArgLeuArgAlaArgMetGluGlu 220
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RESULT 2

E00823
LOCUS
DEFINITION DNA sequence coding for human apolipoprotein E and its signal peptide.
E00823
ACCESSION
VERSION E00823.1 GI:2169084
KEYWORDS JP 1986096997-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.

E00823 1110 bp DNA linear PAT 29-SEP-1997
DNA sequence coding for human apolipoprotein E and its signal peptide.

REFERENCE 1 (bases 1 to 1110)
AUTHORS Teranishi, Y., Matsui, Y., Ikeda, Y. and Kimura, M.
TITLE PRODUCTION OF HUMAN APOLIPOPROTEIN E-LIKE PROTEIN
JOURNAL Patent: JP 1986096997-A 1 15-MAY-1986;
COMMENT MITSUBISHI CHEM IND LTD
OS Human (Homo sapiens)
PN JP 1986096997-A/1
PD 15-MAY-1986
PF 16-OCT-1984 JP 1984216987
PI TERANISHI YUTAKA, MATSUI YASUSHI, IKEDA YASUKO, KIMURA MASAKO
PC C12P21/00,A61K35/74,A61K37/04,C12N15/00,C12P21/00,C12R1:19;
PC C12R1:19;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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FH Key Location/Qualifiers
FT 3'UTR 1..14
FT sig_peptide 15..68
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FT CDS 69..968
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FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 1.04e-120 Length: 1110
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-827-854A-2 (1-299) x E00823 (1-1110)

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QY 21 GlnSerGlyGlnArgTrrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 129 CAGAGCGCGCAGCGCTGGAACTGGCACTGGGTGCTTTTGGGATTAACCTGCGCTGGGTG 189
QY 41 GlnThrLeuSerGluGlnValGlnGluLeuSerSerGlnValThrGlnGluLeu 60
Db 189 CAGACACTGTCTGAGCAGGTGTCAGAGGAGCTGCTCAGCTCCCAAGGTCAACCCAGAACTG 248
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 249 AGGCGCGTGTAGCAGCAGACCATGAAGAGTTGAAGGCCCTACAAATCGGAATCGAGGAA 308
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaLeuSerLysGluLeuGlnAlaAla 100
Db 309 CAACGTACCCCGGTGGCGGAGGACCGCGGCAGCGCTGTCCAAGAGCTGCAGGCGCGC 368
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 369 CAGCGCGCGTGGCGCGGACATGGAGGACGTGTGCGCGCCCTGCTGCTACGTACCGCGC 428
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluLeuLeuArgValArgLeuAlaSerHis 140
Db 429 GAGGTGCAGGCCATGCTCGGCCAGACCCGAGAGCTGCGGGTGCCTGCTCCCTCCAC 488
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 489 CTGCGCNAAGTGGTAGCGGCTCTCCGCGATGCCATGACCTGCAGAGCGCTGCA 548
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
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QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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Db 669 CAGCGCTACAGAGCGCGCGCGCGCGCTGGCGCGCGCGCTGCGCGCGCGAGAG 728
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QY 241 AlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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DEFINITION Sequence 63 from Patent WO0175177.
ACCESSION AX302545
VERSION AX302545.1 GI:17383082
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
Morin, P.J., Sherman-Baust, C.A., Pizer, E.S. and Hough, C.D.
Tumor markers in ovarian cancer
Patent: WO 0175177-A 63 11-OCT-2001;
JOURNAL

THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES Location/Qualifiers
source 1. .1147
/organism="Homo sapiens"
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ORIGIN

Alignment Scores:
Pred. No.: 1.08e-120 Length: 1147
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
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US-09-827-854A-2 (1-299) x AX302545 (1-1147)

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Db 280 AGGCGCGTGTAGCAGGACCATGAAGAGTTGAAGGCCCTACAAATCGGAATCGAGGAA 339
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Db 520 CTGCGCAAGCTGGCTAAGCGGCTCTCCGCGATGCCGATACCTGTCAGAAAGCGCTGGCA 579
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
Db 580 GTGTACAGCGCGCGCGCGCGGCGCGCGCGCGCTTCAGCGCGCTTCAGCGCGCGCGC 639
QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
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 DEFINITION Sequence 12 from Patent WO2004076613.
 ACCESSION CQ875269
 VERSION CQ875269.1 GI:52748357
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1

AUTHORS Herr,A., Hinzmann,B., Dahl,E., Staub,E., Pilarsky,C. and Specht,T.
 TITLE Human nucleic acid sequences from carcinomas of the bladder
 JOURNAL Patent: WO 2004076613-A 12 10-SEP-2004;
 Herr, Alexander (DE); Hinzmann, Bernd (DE); Dahl, Edgar (DE);
 Staub, Elke (DE); Pilarsky, Christian (DE); Specht, Thomas (DE)
 FEATURES
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 Pred. No.: 1.09e-120 Length: 1156
 Score: 1493.00 Matches: 299
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0
 US-09-827-854A-2 (1-299) x CQ875269 (1-1156)
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Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTyrAlaGlyLeuVal 280

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RESULT 9

CQ981476

LOCUS CQ981476

DEFINITION Sequence 331 from Patent EP1498424.

ACCESSION CQ981476

VERSION CQ981476.1

KEYWORDS 1156 bp DNA linear PAT 25-JAN-2005

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1

REFERENCE

AUTHORS Rosenthal, A., Hermann, K., Heiden, E., Pilarsky, C., Bruemendorf, T., Staub, E., Roepcke, S., Mennerich, D., Kinnemann, H. and Li, X.

TITLE Human nucleic acid sequences from lung tumours

JOURNAL Patent: EP 1498424-A 331 19-JAN-2005;

Hinzmann, Bernd (DE); Hermann, Klaus (DE); Heiden, Esmeralda (DE); Rosenthal, Andre (DE)

FEATURES

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Location/Qualifiers

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Alignment Scores:

Pred. No.: 1,09e-120 Length: 1156

Score: 1493.00 Matches: 299

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 2 Gaps: 0

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Db 175 CAGAGCGCGCCAGCGCTGGGAACTGGCACTGGGTGCTTTTGGGATTACTCGCGCTGGGTG 234

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Db 235 CAGACACTGCTGTGAGCAGGTGCAGGAGGAGTGTCTCAGCTCCAGGTCAACAGGAACTG 294

Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80

Db 295 AGGGCGCTGATGGACGAGACCATGAAGGAGTTGAAGGCTTCAAAATCGGAATCGAGGAA 354

Qy 81 GlnLeuThrProValAlaGluGlnThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100

Db 355 CAACCTGACCGCGCTGGCGAGGAGACGCGGCGCATCGGCTGTCCAAGGAGCTGCAGCGCGG 414

Qy 101 GlnAlaArgLeuGluAlaAspMetGluAspValCysGlyArgGluValGlnTyrArgGly 120

Db 415 CAGGCGCGCTGGGCGCGGACATGAGGACGTGTGCGGCGCGCTGTGGTACGATCCGCGCGG 474

Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140

Db 475 GAGGTGCAGGCGCATGCTCGGCCAGACCGAGGAGCTGGGTGCGCTCCGCTCCAC 534

Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAlaAspAlaAspLeuGlnLysArgLeuAla 160

Db 535 CTGGCGCAAGCTGCTTAAGCGGCTCTTCGCGCATGCGGATGACCTGCAGAAAGCGCTGGCA 594

Qy 161 ValTyrGlnAlaGlyAlaArgGluGlnValGlnGluLeuSerLysGluLeuAlaAlaArg 180

Db 595 GTGTACACGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGGCGGCGGCGG 654

Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlnLysSerLeuAlaGly 200

Db 655 CTGGGCGCGCTGGTGGAAACAGGCGCGCTGCGGCGCGGCGCGGCGCGGCGGCGGCGG 714

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Db 835 GCCAAGCTGGAGGACGCGCCAGCAGATAGCGCTGCAGGCGGCGGCTTCCAGCGCGCG 894

Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTyrAlaGlyLeuVal 280

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Qy 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 235 CAGACACTGTCTGAGCGAGGTGCAGAGGAGGTCTCAGCTCCAGGTCAACCCAGGAACCTG 294

Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 295 AGGCGCTGTGATGGACGAGACCATCAAGAGAGTTGAAGGCTTACAAATCGGAACCTGGAGAA 354

Qy 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 775 ATGGGCGAGCGGACCCCGCGCGCTGGACGAGGTGAAGGAGAGGTGGCGGAGGTGGCG 834

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VERSION AX821568.1 GI:39724945
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Turcatti,G.
Nucleotide detection by fluorescence resonance energy transfer and
methods thereof
JOURNAL Patent: WO 03068986-A 1 21-AUG-2003;
Applied Research Systems ARS Holding N.V. (AN)
FEATURES
Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 1,09e-120 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-827-854A-2 (1-299) x AX821568 (1-1156)

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Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
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Db 235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGTCTCAGCTCCAGGTCAACCCAGGAACCTG 294

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Db 355 CAACCTGACCCCGGTGGCGGAGAGCGCGGCGAGCTGTCCAAGGAGCTGCAGCGCGCG 414

Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
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Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
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Qy 241 AlalysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
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DEFINITION Homo sapiens preapolipoprotein E (APOE) mRNA, complete cds.
ACCESSION K00396
VERSION K00396.1 GI:178850
KEYWORDS apolipoprotein E; lipoprotein; polymorphism; very low density lipoprotein.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eumetazoa; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 355 to 1156)
Breslow,J.L., McPherson,J., Nussbaum,A.L., Williams,H.W., Lofquist-Kahl,F., Karathanasis,S.K. and Zannis,V.I. Identification and DNA sequence of a human apolipoprotein E cDNA clone
J. Biol. Chem. 257 (24), 14639-14641 (1982)
6897404
REFERENCE 2 (bases 250 to 777)
Wallis,S.C., Rogne,S., Gill,L., Markham,A., Edge,M., Woods,D., Williamson,R. and Humphries,S. The isolation of cDNA clones for human apolipoprotein E and the detection of apoE RNA in hepatic and extra-hepatic tissues
EMBO J. 2 (12), 2369-2373 (1983)
6199196
REFERENCE 3 (bases 1 to 1156)
Zannis,V.I., McPherson,J., Goldberger,G., Karathanasis,S.K. and Breslow,J.L. Synthesis, intracellular processing, and signal peptide of human apolipoprotein E
J. Biol. Chem. 259 (9), 5495-5499 (1984)
6325438
REFERENCE 4 (bases 88 to 1156)
McLean,J.W., Elshourbagy,N.A., Chang,D.J., Mahley,R.W. and Taylor,J.M. Human apolipoprotein E mRNA. cDNA cloning and nucleotide sequencing of a new variant
J. Biol. Chem. 259 (10), 6498-6504 (1984)
6327682
REFERENCE 5 (bases 577 to 624)
Gill,L.L., Peoples,O.P., Pearson,D.H., Robertson,F.W., Humphries,S.E., Cumming,A.M. and Hardman,N. Isolation and characterisation of a variant allele of the gene for human apolipoprotein E
Biochem. Biophys. Res. Commun. 130 (3), 1261-1266 (1985)
2992507
REFERENCE 6 (sites)
Rall,S.C. Jr., Newhouse,Y.M., Clarke,H.R., Weisgraber,K.H., McCarthy,B.J., Mahley,R.W. and Bersot,T.P. Type III hyperlipoproteinemia associated with apolipoprotein E phenotype E3/3. Structure and Genetics of an apolipoprotein E3 variant
J. Clin. Invest. 83 (4), 1095-1101 (1989)
2539388
COMMENT [1] corrected in [J. Biol. Chem. 258, 11422-11422 (1983)]. [J. Biol. Chem. 258, 11422-11422 (1983)] correction of [1]. [4] epsilon-3 and variant.
[5] epsilon-2 allele.
[6] sites; mutations resulting in type III hyperlipoproteinemia. Apo E is a component of normal human very low density lipoprotein. There are six human apo E phenotypes known to result from a single structural gene, three of the common alleles being epsilon-4, epsilon-3 and epsilon-2. This sequence appears to be of the epsilon-3 allele. [1] argues that the apo E polymorphism involves mutations in the structural coding region; for example the epsilon-2 phenotype which is characterized by hyperlipoproteinemia is thought to result from a c to t change (arg to cys) at base 586 below [3], [5]. The sequence shown is 57% homologous with human apo A-I and 81% homologous with rat apo E. For the epsilon-4 sequence,

see the separate entry.
[J. Biol. Chem. 258, 11422-11422 (1983)] is too extensively revised relative to [1] to record the revisions in the FEATURES table. The sequence below is that of [J. Biol. Chem. 258, 11422-11422 (1983)] and [3].
Apo E is located on chromosome 19 --Jackson, Bruns and Breslow, PNAS USA 81, 2945-2949 (1984) -- and is believed to be linked to the Apo C-II gene (see separate entry).
The two mutations causing type III hyperlipoproteinemia (apolipoprotein E phenotype E3/3) produces substitutions of Arg for Cys at amino acid 112 and Cys for Arg at amino acid position 142. Draft entry and printed copy of sequence for [1] kindly provided by L.L. Gill, University of Aberdeen.
Complete source information:
Human liver [1], [J. Biol. Chem. 258, 11422-11422 (1983)], [2], [3], [4] and blood [5], cDNA to mRNA.
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Alignment Scores:
Pred. No.: 1.09e-120 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
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DB: 5 Gaps: 0

US-09-827-854A-2 (1-299) x HUMAPOE3 (1-1156)

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Qy 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
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Db 655 CTGGGGCCCTCTGGTGGAAACAGGGCGCGTGGGGCCGCCACTGTGGGCTCCCTGGCGGC 714
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Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
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RESULT 14

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ACCESSION BC003557
VERSION BC003557.1 GI:13097698
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominiidae; Homo.
1 (bases 1 to 1186)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Sapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schecterson, F.E., Brownstein, M.J., Ustin, I.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunatratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A.G., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Snailus, D.E.,
Schnurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932

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TITLE
JOURNAL
PUBMED

FEATURES
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ORIGIN

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US-09-827-854A-2 (1-299) x AR531680 (1-1291)

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Qy	21	GlnSerGlyGlnArgTrpGluLeuAlaLeuGluValPheTrpAspTyrLeuArgTrpVal	40
Db	300	CAGAGCGCCAGACCGCTGGGAACCTGGCACTGGGTTCGCTTTGGGATTACCTGCGCTGGGTG	359
Qy	41	GlnThrLeuSerGluGlnValGlnGluGluLeuSerSerGlnValThrGlnGluLeu	60
Db	360	CAGACACTGCTGAGCAGGTGCAGAGGAGCTGCTCAGCTCCACAGGTCAACCAGGAAC TG	419
Qy	61	ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu	80
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Qy	81	GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla	100
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Qy	101	GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly	120
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Qy	121	GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis	140
Db	600	GAGGTGCAGGCCATGCTCGGCCAGACACCAGGAGCTGCGGGTGCCTCGCTCCAC	659
Qy	141	LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla	160
Db	660	CTGCGCAAGCTGCGTAAGCGGCTCCTTCGCGATGCCATGACCTGCAGAAAGCGCCCTGCA	719
Qy	161	ValTyrGlnAlaGlyAlaArgGluGlyValAlaGluArgGlyLeuSerAlaIleArgGluArg	180
Db	720	GTGTACCGCGCGGGGCGCGGAGGCGCGGAGCGCGCTCAGCGCCATCCGCGAGCGC	779
Qy	181	LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly	200
Db	780	CTGGGGCCCTGTGTGAACAGGGCGCGCTGCGGCCCGCCACTGTGGGCTCCTGGCGCGC	839
Qy	201	GlnProLeuGlnArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu	220
Db	840	CAGCCGCTACAGGAGCGGGGCCAGGCTTGGGGCGAGCGGCTGCGCGCGGATGGAGAG	899
Qy	221	MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg	240
Db	900	ATGGGACGCGGACCCCGGACCGCTGGACGAGGTGAAGGAGCAGGTGGCGGAGTGGC	959
Qy	241	AlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg	260
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Qy	261	LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal	280
Db	1020	CTCAAGAGCTGGTTCGAGCCCTCGTGGAGACATGACGCGCCAGTGGCGCGGCTGGTG	1079
Qy	281	GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis	299

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 18:51:12 ; Search time 1029.05 Seconds

(without alignments)
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Perfect score: 1493

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Total number of hits satisfying chosen parameters: 10489840

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1493	100.0	954	14	Adv42852 Human psy
3	1493	100.0	1110	1	AAN60409 Human apo

4	1493	100.0	1147	5	ABA83113	AbA83113 Apolipop
5	1493	100.0	1154	13	ADQ86961	AdQ86961 Human tum
6	1493	100.0	1156	4	AAF84315	AaF84315 Human apo
7	1493	100.0	1156	6	ABT13008	ABt13008 Human apo
8	1493	100.0	1156	6	AAD22048	AaD22048 Human apo
9	1493	100.0	1156	8	ACA64743	AcA64743 Apolipop
10	1493	100.0	1156	8	ACC49103	ACC49103 Human apo
11	1493	100.0	1156	9	ACC84919	ACC84919 Human apo
12	1493	100.0	1156	9	ADA14198	AdA14198 Human apo
13	1493	100.0	1156	10	ADF43409	AdF43409 Apolipop
14	1493	100.0	1156	11	ADI31681	AdI31681 Human CDN
15	1493	100.0	1156	11	AE86465	AeB6465 Human apo
16	1493	100.0	1156	12	ADM41255	AdM41255 Human apo
17	1493	100.0	1156	12	ADN03955	ADn03955 Antipso
18	1493	100.0	1156	13	ACN40622	Acn40622 Tumour-as
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ALIGNMENTS

RESULT 1

AAD26035

ID AAD26035 standard; cDNA; 954 BP.

XX AAD26035;

AC AAD26035;

XX 26-MAR-2002 (first entry)

DT Human apolipoprotein E (APOE) cDNA.

XX Human; antilipaeamic; neuroprotective; nootropic variant; APOE;

XX apolipoprotein E; haplotyping; familial dysbetalipoproteinaemia; therapy;
XX genotyping; type III hyperlipoproteinaemia; Alzheimer's disease; SNP;
XX atherosclerosis; single nucleotide polymorphism; chromosome 19q13.2; ss.

OS Homo sapiens.

XX Key

PH CDS

FT Location/Qualifiers

FT 1..954

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PF 04-JUN-2004; 2004WO-US017686.
 PR 04-JUN-2003; 2003US-0475915P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Nicholson A, Vernon SD;
 PI WPI; 2005-031682/03.
 DR
 XX New microarray comprising probes for genes involved in
 PT psychoneuroendocrine (PNI) activity, useful in diagnosing a
 PT condition associated with PNI activity, e.g., inflammatory or infectious
 PT diseases.
 XX
 PS Claim 1; SEQ ID NO 480; 254pp; English.
 XX
 CC The invention relates to a new microarray which comprises probes for
 CC genes involved in psychoneuroendocrine (PNI) activity. The
 CC microarray is useful in diagnosing a condition associated with PNI
 CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
 CC cancer and infection. The present sequence represents a
 CC psychoneuroendocrine gene expressed sequence tag. Note the
 CC specification mentions SEQ ID NO of up to 3314 but only sequences up to
 CC SEQ ID NO 1829 are provided.
 XX
 SQ Sequence 954 BP; 168 A; 290 C; 377 G; 119 T; 0 U; 0 Other;
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 Pred. No.: 9.13e-107 Length: 954
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 Query Match: 100.0% Indels: 0
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US-09-827-854A-2 (1-299) x ADV42852 (1-954)

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 Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
 Db 115 CAGAGCGGCACGCTGGGAACCTGGCACTGGGTGGCTTTGGGATTACCTGGCTGGGTG 174
 Qy 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
 Db 175 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCAGTCCAGGCAGGAACTG 234
 Qy 61 ArgAlaLeuMetAspGluThrMetIysGluLeuIysAlaTyrLysSerGluLeuGluGlu 80
 Db 235 AGGGCGCTGATGGACGAGACCATGAAGAGGTGAAGGCTTACAAATCGGAACCTGGAGAA 294
 Qy 81 GlnLeuThrProValAlaGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
 Db 295 CAACCTGACCCGGTGGCGAGAGAGCGCGGACCGCTGTCCAGGAGCTCAGCGCGCG 354
 Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
 Db 355 CAGGCCCGCTGGGCGCGGACATGAGGACGTGTGCGGCCGCTGGTGCAGTACCGCGCG 414
 Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
 Db 415 GAGGTGACAGGCCATGCTCGGCCAGAGCACCAGGAGCTGCGGGTGCCTCGCTCCAC 474
 Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
 Db 475 CTGGCAAGCTGCGTGAAGCGCTCTCCCGCATGCCGATGACCTGCAGAACGCGCTGGCA 534
 Qy 161 ValTyrGlnAlaGlyAlaArgGluGlyValaGluArgGlyLeuSerAlaIleArgGluArg 180
 Db 535 GTGTACCAAGGCCGGGCGCGAGGGCGCGAGCGCGGCGCTCAGCGCCATCCGCGAGCGC 594

Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
 Db 595 CTGGGGCCCCCTGGTGGAAACAGGGCGCGGTGGGGCCGCCACTGTGGGCTCTCTGGCCGCG 654
 Qy 201 GlnProLeuGlnArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
 Db 655 CAGCCGCTACAGGAGCGGCCACAGGCTTGGGGCGAGCGGCTGCGCGCGGATGGAGGAG 714
 Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
 Db 715 ATGGGACGCGGACCCCGACCGCTGGACAGGTGAAGGAGCAGGTGGCGAGGTGCGC 774
 Qy 241 AlalysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
 Db 775 GCCAAGCTGGAGGAGCGGCCACAGCAGATAGCTTCAGGCGGAGGCTTCAGGCCGCGC 834
 Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
 Db 835 CTCAGAGCTGGTTCGAGCCCTGGTGAAGACATGCAGCGCCAGTGGCGCGGCTGGTG 894
 Qy 281 GluLysValGlnAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
 Db 895 GAGAAAGTGCAGGCTGCGGTGGGCACCGAGCGGCCCTGTGCGCCAGCGCAATCAC 951

RESULT 3
 AAN60409
 ID AAN60409 standard; DNA; 1110 BP.
 XX
 AC AAN60409;
 XX
 DT 25-MAR-2003 (revised)
 DT 01-JAN-1980 (first entry)
 XX
 DE Human apolipoprotein-E.
 XX
 KW Apolipoprotein-E; hyperlipidemia; arteriosclerosis; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 15..968
 FT /*tag= a
 XX
 PN AU8547513-A.
 XX
 PD 24-APR-1986.
 XX
 PF 17-SEP-1985; 85AU-00047513.
 XX
 PR 16-OCT-1984; 84JP-00216987.
 PR 11-JUN-1985; 85JP-00126989.
 XX
 PA (MITU) MITSUBISHI CHEM IND LTD.
 XX
 DR WPI; 1986-150217/24.
 DR P-PSDB; AAP60507.
 XX
 PT New DNA sequence coding for human apolipoprotein-E - and expression
 PT vectors and transformed cells contg. it.
 XX
 PS Disclosure; Fig 2; 45pp; English.
 CC
 CC The encoded protein is used to treat subjects who are deficient in
 CC apolipoprotein-E (or who produce abnormal forms of this molecule) and
 CC therefore are likely to suffer from hyperlipidemia, resulting in
 CC arteriosclerosis. It can also be used to raise antisera for detecting the
 CC protein deficiency or production of abnormal forms. (Updated on 25-MAR-
 CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 1110 BP; 198 A; 354 C; 415 G; 143 T; 0 U; 0 Other;
 Alignment Scores:

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Pred. No.: 1.08e-106 Length: 1110
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-09-827-854A-2 (1-299) x AAN60409 (1-1110)
QY 1 LyeValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
Db 69 AAGTGGAGCAGCGGTGGAGCAGAGCCGAGCCGAGCTGCGCCAGCAGACCGAGTGG 128
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 129 CAGAGCGCCAGCGCTGGGNACTGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGG 188
QY 41 GlnThrLeuSerGluGlnValGlnGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 189 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCCGAGGTCCACCCAGGAAC 248
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 249 AGGGCCGCTGATGACGAGACCATGAAGGAGTTGAAGCCCTACAAATCGGAACATGGA 308
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db 309 CAACTGACCCCGTGGCGGAGGAGACCGCGGCACGGCTGTCCAAGGAGCTGCAGGCG 368
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 369 CAGGCGCGGCTGGCGCCGACATGAGAGCGTGTGGCGCGCTGTGGTGCAGTACCGCG 428
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 429 GAGGTGAGGCCATGCTCGGCCAGAGACCGAGGAGCTGGGGTGGCCCTCGCCCTCCCAC 488
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 489 CTGCGCAAGCTGCTGAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGG 548
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaAlaArgGluArg 180
Db 549 GTGTACCAAGCCCGGCGCCGAGGCGCGCGAGCGCGCTCAAGCGCCATCCCGCAGCGC 608
QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 609 CTGGGGCCCTGGTGGAAACAGGGCCGCGTGGCGGCCGCCACTGTGGCTCCCTGGCG 668
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
Db 669 CAGCCGCTACAGAGCGGGCCCGAGGCTGGGGCGAGCGGCTGCGCGCGGATGGAGGAG 728
QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 729 ATGGGCGAGCGGACCCCGCCGCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGGCG 788
QY 241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 789 GCCAAGCTGAGGAGACAGGCCCGCCAGCATAGCTGCGAGGCCGAGGCTTCCAGGCCCG 848
QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db 849 CTCAGAGCTGGTTCGAGCCCTTGGTGAAGACATGCAGCGCCAGTGGGCGGGCTGGTG 908
QY 281 GluLysValGlnAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 909 GAGAAGGTGAGGCTGCGGTGGGCACGAGCGCCGCTGTGGCCGACCAATCAC 965

RESULT 4
ABA83113
ID ABA83113 standard; DNA; 1147 BP.
XX
```

```
AC ABA83113;
XX 08-FEB-2002 (first entry)
XX Apolipoprotein E ovarian tumour marker gene, SEQ ID NO:63.
XX
KW Ovarian tumour marker gene; human; overexpression; upregulation;
KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;
KW identification; serous cystadenoma; borderline serous tumour;
KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;
KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;
KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;
KW immune response pathway; cell proliferation regulation; protein folding;
KW membrane localised; secreted; therapeutic target; cytostatic;
KW gene therapy; vaccine; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200175177-A2.
XX
XX 11-OCT-2001.
XX
XX 03-APR-2001; 2001WO-US010947.
XX
XX 03-APR-2000; 2000US-0194336P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;
XX
XX WPI; 2001-626450/72.
XX
XX P-PSDB; ABB50287.
XX
XX Detecting and identifying ovarian tumor, identifying increased risk for
XX developing ovarian cancer, and determining effectiveness of ovarian
XX cancer treatment, by measuring expression level of ovarian tumor marker
XX gene.
XX
XX Claim 23; Page 105-106; 140pp; English.
XX
XX The invention relates to methods for diagnosing and prognosing ovarian
XX tumors in an individual via the detection and measurement of the
XX expression of ovarian tumor marker genes (ABA83081-ABA83122, ABA83180,
XX ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,
XX ABA83181 and ABA83183). The methods of the invention are useful for
XX detecting an ovarian tumor in a patient, for identifying an individual
XX at increased risk for developing ovarian cancer, in prognostic tests for
XX assessing the relative severity of ovarian cancer, in tests for
XX monitoring a patient in remission from ovarian cancer and in tests for
XX monitoring disease status in a patient being treated for ovarian cancer.
XX The methods can additionally be used to identify a particular tumor as
XX being an ovarian tumor (i.e., an epithelial ovarian tumor selected from
XX serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,
XX mucinous cystadenoma, borderline mucinous tumour, mucinous
XX cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,
XX clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner
XX tumour. The ovarian tumor marker genes of the invention were identified
XX using SAGE (serial analysis of gene expression) and were found to be
XX overexpressed in a broad variety of ovarian epithelial tumour cells
XX relative to normal ovarian epithelial cells. The marker genes are
XX implicated in immune response pathways, in the regulation of cell
XX proliferation and in protein folding, and many of these are membrane-
XX localised or secreted. In addition to their use as diagnostic and
XX prognostic markers, the ovarian tumor marker genes or their encoded
XX proteins may be used as therapeutic targets for the treatment and
XX prevention of ovarian cancer. Sequences ABA83081-ABA83122, ABA83180,
XX ABA83182 and ABA83184 represent the ovarian tumour marker genes of the
XX invention
XX
XX Sequence 1147 BP; 210 A; 365 C; 425 G; 147 T; 0 U; 0 Other;
XX
XX Alignment Scores:
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Pred. No.:	1.12e-106	Length:	1147
Score:	1493.00	Matches:	299
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0
US-09-827-854A-2 (1-299) x ABA83113 (1-1147)			
Qy	1	LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp	20
Db	100	AAGGTGGAGCAAGCGGTGGACACAGCGCGAGCGCGAGCTGCCACGACACCGAGTGG	159
Qy	21	GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal	40
Db	160	CAGAGCGCGACCGCTGGAACTGGCACTGGGTGCTTTGGGATTACCTGGCTGGGTG	219
Qy	41	GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu	60
Db	220	CAGACACTGTCTGAGCAGGTGCAGGAGGAGTGTCTCAGCTCCAGGTCACCCAGGAAC	279
Qy	61	ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu	80
Db	280	AGSGCGCTGTGGACGACCATGAAGGAGTTGAAGGCTTCAAAATCGAACTGGAGGA	339
Qy	81	GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAla	100
Db	340	CAACTGACCCCGTGGCGAGAGACGCGCGACGCTGTCCAGGAGCTGCAGCGCGC	399
Qy	101	GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly	120
Db	400	CAGSCCGCTGGCGCGGACATGAGGAGCGTGTGGCGCGCTGGTGCAGTACCGCGC	459
Qy	121	GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis	140
Db	460	GAGGTGCAGGCGCATGCTCGGCAGACACCGAGGAGTGGCGGTGCGCTCCCTCCAC	519
Qy	141	LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla	160
Db	520	CTGGCGAAGCTGGCTAAGCGGCTCTCTCGCGATGCGGATGACCTGCAGAACGCTGGCA	579
Qy	161	ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg	180
Db	580	GTGTACACAGCGCGGCGCGAGGCGCGCGCGCGCTCAGCGCATCCGCGAGCGC	639
Qy	181	LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly	200
Db	640	CTGGGCGCTTGGTGGAAACAGGCGCGCTGCGGCGCGCACTGTGGGTCTCCCTGGCGGC	699
Qy	201	GlnProLeuGlnAlaArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu	220
Db	700	CAGCGCTTACAGAGCGGCGCGCGCGCGCGCGCGCGCTGCGCGCGGATGAGAG	759
Qy	221	MetGlySerArgTrpArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg	240
Db	760	ATGGGACCGGACCGCGCGCGCTGGACGAGGTGAAGGAGCAGGTGGCGAGGTGGC	819
Qy	241	AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg	260
Db	820	GCCAAAGTGGAGGAGCAGGCGCGCAGCAGATAGCTTCAGGCGCGAGGCTTCCAGGCGCGC	879
Qy	261	LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal	280
Db	880	CTCAAGAGCTGTTCGAGCGCTTGTGGAAACATATGACGCGCGCTGGCGCGCGCTGGT	939
Qy	281	GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis	299
Db	940	GAGAGGTGCGAGGTGCGTGGGACCGACGCGCGCGCTGTGGCCGAGGACAAATCAC	996

RESULT 5

ADQ86961

ID ADQ86961 standard; cDNA; 1154 BP.

XX

AC	ADQ86961;
XX	07-OCT-2004 (first entry)
DT	Human tumour-associated antigenic target (TAT) cDNA sequence #3836.
XX	human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
DE	cancer; cell proliferative disorder; gene; ss.
KW	Homo sapiens.
XX	WO2004060270-A2.
XX	22-JUL-2004.
XX	15-OCT-2003; 2003WO-US029126.
XX	18-OCT-2002; 2002US-0418988P.
XX	(GETH) GENENTECH INC.
PA	(WUTD/) WU T D.
PA	(ZHOU/) ZHOU Y.
XX	Wu TD, Zhou Y;
XX	WPI; 2004-534300/51.
DR	New nucleic acid molecule and encoded polypeptide, for diagnosing,
XX	preventing or treating cell proliferative disorders such as cancer.
PT	Claim 1; SEQ ID NO 3836; 5504pp; English.
XX	The present invention describes an isolated tumour-associated antigenic
CC	target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC	sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC	(a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC	sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC	(c). Also described: (1) an expression vector comprising the above
CC	nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC	a process for producing a polypeptide; (4) an isolated polypeptide
CC	comprising: (a) an amino acid sequence encoded by any of the above
CC	nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC	length coding region of the above nucleotide sequences; or (c) a sequence
CC	having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC	comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC	an isolated antibody that binds to the above polypeptide; (7) a process
CC	for producing the antibody; (8) an isolated oligopeptide that binds to
CC	the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC	binding organic molecule that binds to the above polypeptide; (10) a
CC	composition of matter comprising the above (chimeric) polypeptide,
CC	antibody, oligopeptide or TAT binding organic molecule, in combination
CC	with a carrier; (11) an article of manufacture comprising a container and
CC	the composition of matter contained within the container; (12) methods of
CC	inhibiting the growth of a cell that expresses the above protein, where
CC	the growth of the cell is at least in part dependent upon a growth
CC	potentiating effect of the above protein; (13) a method of
CC	therapeutically treating a mammal having a cancerous tumour comprising
CC	cells that express the above protein; (14) a method of determining the
CC	presence of a protein in a sample suspected of containing the protein
CC	described above; (15) methods of diagnosing the presence of a tumour in a
CC	mammal; (16) a method for treating or preventing a cell proliferative
CC	disorder associated with increased expression or activity of the above
CC	protein; and (17) a method of binding an antibody, oligopeptide or
CC	organic molecule to a cell that expresses the protein described above.
CC	The TAT sequences have cytostatic activities, and can be used in gene
CC	therapy. The composition and methods are useful for diagnosing,
CC	preventing or treating cancer. The composition is also used for preparing
CC	a medicament for the therapeutic treatment or diagnostic detection of a
CC	cell proliferative disorder or cancer. The present sequence represents a
CC	human TAT cDNA sequence from the present invention.
XX	Sequence 1154 BP; 208 A; 367 C; 431 G; 148 T; 0 U; 0 Other;
XX	Sequence 1154 BP; 208 A; 367 C; 431 G; 148 T; 0 U; 0 Other;

Db	415		CAGGCCCGCGCTGGGCGCGGACATGAGAGACGTGTGCGCGCTGGTGAGTACGCGCGC	474
Qy	121		GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuAtrgValArgLeuAlaSerHis	140
Db	475		GAGGTGAGGCGCATGCTCGGCACAGACACCGAGGAGCTGCGGCTGGCGCTCCCTCCAC	534
Qy	141		LeuArgTysLeuAtrgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla	160
Db	535		CTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAAAGCGCTGGCA	594
Qy	161		ValTyrGlnAlaGlyAlaArgGluGlyAlaGluAtrgGlyLeuSerAlaIleArgGluAtrg	180
Db	595		GTGTACCAAGCGCGGGCCCGAGGCGCGCGAGCGCGCTCAGCGCCATCCGCGAGCGC	654
Qy	181		LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly	200
Db	655		CTGGGGCCCTGTGTGGACAGGGCCGCTGCGGGCGCGCATGTGTGGCTCCCTGCGCGC	714
Qy	201		GlnProLeuGlnGluAtrgAlaGlnAlaTrpGlyGluAtrgLeuArgAlaArgMetGluGlu	220
Db	715		CAGCCGCTACAGGACGGGCGCCAGGCGTGGGCGAGCGCTGCGCGCGCGATGAGGAG	774
Qy	221		MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluAtrg	240
Db	775		ATGGGACGCGGACCCGCGCGCTGACGAGGTGAAGGACAGGTGTCGCGAGGTGGC	834
Qy	241		AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg	260
Db	835		GCCAAGCTGGAGGAGCAGGCGCCAGCAGATACGCTGCGAGCGCGAGGCTTCAGGCGCGC	894
Qy	261		LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal	280
Db	895		CTCAAGAGCTGTTTCGAGCCCTCTGTGTGAAGACATGCAGCGCGCAGTGGCGCGGTGGT	954
Qy	281		GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspSerHis	299
Db	955		GAGAAAGGTGCAGGTGCGCTGGGCACAGCGCGCCCTGTGTCGCCAGCGACAATCAC	1011
RESULT 7				
Db	ABT13008	ABT13008 standard; DNA; 1156 BP.		
XX	AC	ABT13008;		
XX	DT	30-JAN-2003 (first entry)		
XX	XX	Human apolipoprotein E (APOE) gene.		
KW	KW	Human; gene; ds; gene therapy; single nucleotide polymorphism; SNP;		
KW	KW	cytochrome C oxidase subunit Vb; COX6B; high serum cholesterol; GPI-1;		
KW	KW	N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;		
KW	KW	glycosylphosphatidylinositol-1; low serum high density lipoprotein.		
OS	OS	Homo sapiens.		
XX	XX	Location/Qualifiers		
FT	FT	Key variation	replace(197, C)	
FT	FT		/*tag= a	
FT	FT		/note= "Single nucleotide polymorphism"	
FT	FT	variation	replace(448, C)	
FT	FT		/*tag= b	
FT	FT		/note= "Single nucleotide polymorphism"	
FT	FT	variation	replace(540, T)	
FT	FT		/*tag= c	
FT	FT		/note= "Single nucleotide polymorphism"	
FT	FT	variation	replace(586, T)	
FT	FT		/*tag= d	
FT	FT		/note= "Single nucleotide polymorphism"	
XX	PN	MO200272604-A2.		
XX	PD	19-SEP-2002.		

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QY 141 LeuArgGlyLeuArgGlyArgGlyLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
DB 535 CTGCGCAAGCTGGTAAGCGCTCTCCGCGATGCCGATGCACCTGCAGAAGCGCTGGCA 594
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaLeuArgGluArg 180
DB 595 GTGTACAGCGCGGGCCCGCGAGGGCGCGAGCGCGCTCAGCGCCATCCGCGAGCGC 654
QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
DB 655 CTGGGGCCCTGTGTGAACAGGGCCGCGTGGGGCCGCCACTGTGGGCTCCCTGGCGCGC 714
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
DB 715 CAGCCGCTACAGAGCGGGCCAGCGCTGGGGCGAGCGCTGCGCGCGGATGGAGGAG 774
QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
DB 775 ATGGGAGCGCGGACCGCGACCGCTGGACGAGGTGAAGGAGCGAGGTGGCGAGGTGCGC 834
QY 241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
DB 835 GCCAAGCTGAGAGAGAGCGGCCCGAGCATACGCTGCAGGCCCGAGGCTTCCAGGCCCGC 894
QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
DB 895 CTCAGAGAGCTGGTTCCGAGCGCCCTGGTGAAGACATGCAGCGCCAGTGGGCGCGCTGGTG 954
QY 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAlaHis 299
DB 955 GAGAAAGTGCAGGCTGCGTGGGACAGCGCGCCCTGTGCCAGCGCAATCAC 1011
RESULT 8
AAD22048
ID AAD22048 standard; DNA; 1156 BP.
XX
AC AAD22048;
XX
DT 12-FEB-2002 (first entry)
XX
DE Human apolipoprotein E (apoE) isoprotein, apoE3 DNA.
XX
KW Human; apolipoprotein E; apoE; cholesterol; atherosclerosis;
KW hypertriglyceridaemia; low density lipoprotein; LDL; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 61..1014
FT FT /*tag= a
FT FT /product= "Human apoE isoprotein, apoE3"
FT sig_peptide 61..114
FT FT /*tag= b
FT mat_peptide 115..1011
FT FT /*tag= c
FT FT /product= "Mature human apoE isoprotein, apoE3"
XX
XX WO200177136-A1.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-US011358.
XX
XX 06-APR-2000; 2000US-00544386.
XX
XX 04-OCT-2000; 2000US-00679088.
XX
XX 05-APR-2001; 2001US-00827854.
XX
XX (KOSP-) KOS PHARM INC.
XX (UYBO-) UNIV BOSTON.
XX
XX Zannis VI, Kypreos KE;
XX
XX WPI; 2002-010885/01.

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DR P-PSDB; AAE13294.
XX
XX New apolipoprotein E polypeptide and nucleic acid, useful for lowering
PT cholesterol, delaying the onset of or treating atherosclerosis in mammal,
PT without inducing hypertriglyceridemia.
XX
XX Claim 14; Page 81; 91pp; English.
XX
XX The present sequence is a human apolipoprotein E (apoE) isoprotein, apoE3
CC DNA. The apoE lipoproteins are useful for lowering cholesterol, delaying
CC the onset of atherosclerosis, treating or regressing atherosclerosis
CC without inducing hypertriglyceridaemia, in a mammal lacking an
CC endogenous, normally functioning apoE gene or low density lipoprotein
CC (LDL) receptor or is at risk for developing atherosclerosis due to
CC accumulation of lipoprotein remnants in the bloodstream or having a
CC defect in remnant removal
XX
XX Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;
SQ

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Alignment Scores:
Pred. No.: 1,13e-106 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0
US-09-827-854A-2 (1-299) x AAD22048 (1-1156)

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QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnThrGluTrp 20
DB 115 AAGGTGAGCAAGCGGTGGAGACAGAGCGGAGCGCGAGCTGCCGACGAGCCGAGTGG 174
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTyrVal 40
DB 175 CAGAGCGCGCAGCGCTGGGAACCTGGCAGCTGGGTCTTTTGGATTACCTGCCCTGGGTG 234
QY 41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
DB 235 CAGACACTGCTGAGCAGGTGCGAGGAGAGTGTCTCAGCTCCAGGTCCACCCAGGAATG 294
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
DB 295 AGGGCGCTGATGCAGCAGACCATGAAGAGGATTGAAGGCCCTACAAATCGGAATCGGAGAA 354
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
DB 355 CAAGTCAACCCCGTGGCGGAGGAGACCGGGCAGCGCTGTCCAAGGAGCTGCAGGCGCG 414
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
DB 415 CAGGCCCGCTGGCGCGGACATGGAGAGCGTGTGGCGCGCTGTGGTGCAGTACCGCGCG 474
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
DB 475 GAGGTGCAGGCCCATGCTCGGCCAGAGCACCGAGGAGCTGGCGGTGGCGCTGCCCTCCAC 534
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
DB 535 CTGCGCAAGCTGGTAAGCGGCTCTCCGCGATGCCGATGCCTGCAGAGAGCGCTGGCA 594
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaLeuArgGluArg 180
DB 595 GTGTACAGCGCGGGCCCGCGAGGGCGCGAGCGCGCTCAGCGCCATCCGCGAGCGC 654
QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
DB 655 CTGGGGCCCTGTGTGAACAGGGCCGCGTGGGGCCGCCACTGTGGGCTCCCTGGCGCGC 714
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
DB 715 CAGCCGCTACAGAGCGGGCCAGCGCTGGGGCGAGCGCTGCCGCGCGGATGGAGGAG 774

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Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluInValAlaGluValArg 240
Db 775 ATGGGCGAGCCGACCGCGCTGACGAGGTGAAGGACGAGTGGCGGAGGTGGC 834
Qy 241 AlalysLeuGluGluAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 835 GCCAAGCTGGAGGAGCAGGCCACGACGATACGCTTCAGAGCGGAGGCTTCAGGCCCGC 894
Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db 895 CTCAGAGCTGGTTCGAGCCCTGGTGAAGACATGACGACCCAGTGGCGCGGTGGT 954
Qy 281 GlulysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 955 GAGAAGGTGCAGGCTGCGGTGGCACCAAGCGCCGCTGTGCCAGCGACAATCAC 1011

RESULT 9
ACA64743
ID ACA64743 standard; DNA; 1156 BP.
XX
AC ACA64743;
XX
DT 18-JUN-2003 (first entry)
XX
DE Apolipoprotein gene #3.
XX
KW Superantigen; ds; gene; SAg; staphylococcal enterotoxin; tumour; cancer;
KW apoptosis; gene therapy; mammalian cell receptor; cytostatic;
KW tumour associated lipid; energy; T cell; antigen presenting cell; APC;
KW tumouricidal immunocyte; antitumour.
XX
OS Unidentified.
XX
PN US2002177551-A1.
XX
PD 28-NOV-2002.
XX
PF 30-MAY-2001; 2001US-00870759.
XX
PR 31-MAY-2000; 2000US-0208128P.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
WPI: 2003-361759/34.
DR P-PSDB; ABU79141.
XX
PT A mammalian cell receptor, useful in the treatment of cancer by binding
PT to tumor associated lipids where the binding induces energy or apoptosis
PT in T cells and antigen presenting cells.
XX
PS Example 2; Page; 167pp; English.
XX
CC The invention relates to a mammalian cell receptor, useful in the
CC treatment of cancer, which binds to tumour associated lipids and induces
CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
CC Also included are a mammalian cell useful in the treatment of cancer
CC where the receptor which binds tumour associated lipids and induces
CC cellular inactivation or death is deleted or functionally deactivated,
CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
CC (by allowing tumour associated lipids to contact immunocytes in which
CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
CC deleted), a construct useful in the treatment of cancer comprising a
CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
CC useful in the treatment of cancer (where an adaptor protein which
CC inhibits T cell activation by tumour associated antigens is deleted or
CC functionally deactivated), a composition useful in the treatment of
CC cancer (comprising a lipid raft conjugated to a superantigen), producing
CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
CC allowing tumour associated lipids to contact immunocytes, in which
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CC receptors for the lipids are inactivated or deleted to produce a
CC tumouricidal immunocyte population, and administering the tumouricidally
CC activated immunocytes to the host), producing (M3) a tumouricidal APC
CC population ex vivo in a mammal (by allowing a tumour associated lipid to
CC contact APCs, in which receptors for the tumour associated lipids are
CC inactivated or deleted to produce a tumouricidally activated population,
CC and administering APCs to the host), producing a tumouricidal T cell
CC population ex vivo in a mammal) by allowing a tumour associated lipids to
CC contact T cells, in which adaptor proteins which inhibit T cell
CC activation by tumour associated antigens, are deleted or functionally
CC deactivated to produce a tumouricidal population of T cells, and
CC administering the tumouricidally activated T cells to the host, or
CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC administering the tumouricidally activated T cells to the host), treating
CC (M5) cancer in a mammal (by administering a lipid binding molecule which
CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC a tumouricidal T cell population in vivo in a mammal (by allowing a
CC tumour associated antigen to contact immunocytes in which adaptor
CC proteins which inhibit T cell activation by tumour associated antigens
CC are deleted or functionally deactivated) and producing (M7) a
CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC receptors, methods and compositions are useful for treating cancers and
CC tumours. Bacterial superantigens are co-administered or administered as
CC fusion constructs with anti-tumour proteins or motifs. The present
CC sequence encodes an anti-tumour protein which is co-administered with or
CC incorporated into a fusion construct with a superantigen. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from the US patent
CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
XX
SQ Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;
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Alignment Scores:
Pred. NO.: 1.13e-106 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0
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US-09-827-854A-2 (1-299) x ACA64743 (1-1156)

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Qy 1 LysValGluGlnAlaValGluThrGluProGluLeuArgGlnGlnThrGluTrp 20
Db 115 AAGGTGAGGACGAGCGGTGGAGACAGACCGGAGGCCGAGCTGCCACGACAGCGAGTGG 174
Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 175 CAGAGCGCCAGCGCTGGGAACCTGGCTCGCTTTTGGGATTACCTCGCTGGGTG 234
Qy 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 235 CAGACACTGTCTGACGAGGTGCAGGAGGAGTGTCTAGTCCAGGTCCACCCAGGAAC 294
Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 295 AGGCGCTGATGGACGAGACCATGAAGGCTTGAAGGCCTTACAATCGAACTCGAGGAA 354
Qy 81 GlnLeuThrProValAlaGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db 355 CNACTGACCCCGTGGCGGAGGACGCGGCGACGGCTGTCCAAGAGCTGCAGGCGCG 414
Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 415 CAGCCCGGCTGGCGCGGACATGAGAGACGTGTGTGCGGCCCGCTGGTGCAGTACGCGCGC 474
Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 475 GAGGTGCAGGCGCATGCTCGGCCAGAGCACCAGGAGGCTGCGGGTGGCGCTCCCTCC 534
Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
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Db 535 CTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGTCGATGACCTGACGAGCGCCCTGGCA 594
 Qy 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
 Db 595 GTGTACACAGCCCGGCGCCCGAGAGGCGCGAGCGGCTCAGCCGCTCAGCCGAGCGC 654
 Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
 Db 655 CTGGGGCCCCCTGGTGAACACAGGCGCGCTGCGGGCGCCACCTGTGGCTCCCTGGCGCG 714
 Qy 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
 Db 715 CAGCCGCTACAGAGCGGCGCCAGGCTGCGGCGAGCGCTGCGCGCGATGAGGAG 774
 Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValGlyGlnValAlaGluValArg 240
 Db 775 ATGGGAGCGCGGACCCCGGACCCCTGGACGAGGTGAGGAGCAGGTGGCGAGGTGGCG 834
 Qy 241 AlaLysLeuGluGlnGlnAlaGlnGlnIleArgLeuGlnAlaGlnAlaPheGlnAlaArg 260
 Db 835 GCCAAGCTGGAGGAGCAGGCGCCAGCAGATACGCTGCAGGCGCAGGCTTCCAGGCGCGC 894
 Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
 Db 895 CTCAGAGAGCTGGTTCAGAGCCCTGGTGAAGACATGCAGCGCAGTGGCGCGGCTGGTG 954
 Qy 281 GlnLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
 Db 955 GAGAAGGTGAGGCTGCGTGGGACACAGCGCGCCCTGTGCCAGCGCAATCAC 1011
 RESULT 10
 ACC49103
 ID ACC49103 standard; cDNA; 1156 BP.
 XX
 AC ACC49103;
 XX
 DT 18-JUN-2003 (first entry)
 XX
 DE Human apolipoprotein E coding region nucleotide sequence.
 XX
 KW Human; apolipoprotein E; apoE; haplotype; detection; allele; genotype;
 KW multiple haplotypic genetic variation; polymorphism; chromosome 19q13.2;
 KW gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003018835-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 22-AUG-2002; 2002WO-DK000552.
 XX
 PR 23-AUG-2001; 2001DK-00001252.
 XX
 PA (HVID-) HVIDOVRE HOSPITAL.
 XX
 PI Fenger M, Bentzen J;
 XX
 DR WPI; 2003-342453/32.
 XX
 XX
 PT Determining the genetic haplotype of a part of an individual genotype,
 PT comprises determining the presence or absence of specific nucleotide
 PT polymorphisms of a pair of homologous chromosomes.
 XX
 XX Example 3; Page; 56pp; English.
 PS
 CC The present invention describes a method for detecting the presence or
 CC absence of multiple haplotypic genetic variations in a preselected region
 CC of one chromosome of a chromosome pair comprises selecting nucleotide
 CC polymorphisms, suspected to occur in the preselected region, isolating a
 CC target nucleic acid (TNA) of the chromosome pair from a sample, and
 CC detecting the presence or absence of several polymorphisms, using
 CC designed oligonucleotide probes. The method is useful for detecting the

CC presence or absence of multiple haplotypic genetic variations in a
 CC preselected region of one chromosome of a chromosome pair. The method is
 CC also useful for determining the linkage phase between two adjacent loci.
 CC The method is fast, inexpensive and provides uncomplicated determination
 CC of haplotypes in nucleic acid fragments of varying length from 25-40000
 CC base pairs. The present sequence represents the human apolipoprotein E
 CC (apoE) coding region nucleotide sequence, which is used in the
 CC exemplification of the present invention. Human apoE is located on
 CC chromosome 19q13.2. N.B. The present sequence is not given in the
 CC specification but the coding sequence of apoE is referred to in Example
 CC 3 by Genbank accession number K00396
 XX
 SQ Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;
 Alignment Scores: 1.13e-106 Length: 1156
 Pred. No.: 1493.00 Matches: 299
 Score: 1493.00 Conservative: 0
 Percent Similarity: 100.0% Mismatches: 0
 Best Local Similarity: 100.0% Indels: 0
 Query Match: 100.0% Gaps: 0
 DB: 8
 US-09-827-854A-2 (1-299) x ACC49103 (1-1156)
 Qy 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
 Db 115 MAGGTGGAGCAAGCGGTGGAGACAGAGCGGAGCCGAGCTGCGCCAGCAGACCGAGTGG 174
 Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
 Db 175 CAGAGCGCGCAGCGCTGGGAACCTGGGCTGCTTTGGGATTAACCTGGCTGGGTG 234
 Qy 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
 Db 235 CAGACACTGTCTGAGCAGGTGCGAGGAGGAGCTGCTCAGTCTCCAGCTCAGCAGGAATG 294
 Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
 Db 295 AGGGCGCTGATGACGAGACCATGAAGAGGTTGAAGGCCCTACAAATCGGAACCTGGAGAA 354
 Qy 81 GlnLeuThrProValAlaGluGluThrArgAlaArgSerLysGluLeuGlnAlaAla 100
 Db 355 CAACTACCCCGGTGGCGGAGAGACCGCGGACGCTGTCCAAGGAGCTGCAAGCGCGC 414
 Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
 Db 415 CAGGCCCGCTGGCGCGGACATGGAGGACGTGTGCGCGCGCTGTGTGACAGTACCGCGC 474
 Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
 Db 475 GAGGTGCAGGCCATGTCTCGGCCAGACACCGAGAGCTGCGGGTGGCGCTCGCTCCAC 534
 Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
 Db 535 CTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCGGATACCTGCAAGAGCGCTGGCA 594
 Qy 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
 Db 595 GTGTACACAGGCGGCGCGCGAGGCGCGCGAGCGGCTCAGCGCCATCCCGAGCGC 654
 Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
 Db 655 CTGGGGCCCCCTGGTGAACACAGGCGCGCTGCGGGCGCGCCACTGTGGGCTCCCTGGCGCG 714
 Qy 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
 Db 715 CAGCCGCTACAGAGCGGCGCCAGGCTGCGGCGAGCGGCTGCGCGCGATGAGGAG 774
 Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
 Db 775 ATGGCAGCGCGGACCCCGCAGCCCTGGACGAGGTGAAGGAGCAGGTGGCGGAGTGGCG 834
 Qy 241 AlaLysLeuGluGlnGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260

Db 835 GCCAAGCTGAGAGGACGAGCCAGACAGTAGCCCTGCAGGCGGAGGCTTCCAGGCCGCG 894
Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db 895 CTCGAAGAGCTGGTTTCGAGCCCTCGTGGAGACATGCAGGCCAGTGGCGCGCTGGTG 954
Qy 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 955 GAGAAGGTGCAGGCTGCGTGGGACCAGCGCCGCCCTGTGTGCCGAGCAATCAC 1011
RESULT 11
ACC84919
ID ACC84919 standard; DNA; 1156 BP.
XX
AC ACC84919;
XX
DT 03-OCT-2003 (first entry)
XX
DE Human apo E polypeptide encoding DNA.
XX
KW Nuclear hormone receptor ligand; ophthalmological; cholesterol transport;
KW lipid efflux; macular degeneration; apolipoprotein E; apo E; human; gene;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 61..1014
FT /*tag= a
FT /*product= "Apo E"
XX
FN WO2003049685-A2.
XX
PD 19-JUN-2003.
XX
XX 06-DEC-2002; 2002WO-US038856.
XX
XX 07-DEC-2001; 2001US-0340498P.
PR 03-OCT-2002; 2002US-0415864P.
XX
PA (SCHW/) SCHWARTZ D M.
PA (DUNC/) DUNCAN K.
PA (BAIL/) BAILEY K.
PA (KANE/) KANE J.
PA (ISHI/) ISHIDA B.
XX
PI Schwartz DM, Duncan K, Bailey K, Kane J, Ishida B;
XX
XX WPI; 2003-586846/55.
DR P-PSDB; ABR62030.
XX
PT Increasing lipid efflux from and reverse cholesterol transport in ocular
PT tissue used for treating e.g. macular degeneration comprises delivering
PT nuclear hormone receptor ligand.
XX
PS Disclosure; Page 55-56; 97pp; English.
XX
CC The invention relates to increasing lipid efflux from and reverse
CC cholesterol transport in an ocular tissue and involves delivering at
CC least one nuclear hormone receptor ligand. The method is used for
CC increasing lipid efflux and reverse cholesterol transport in ocular
CC tissue, preferably retinal pigment epithelium (RPE) and/or Bruch's
CC membrane, in an individual afflicted with AMD or Stargardt's disease
CC (fundus flavimaculatus), and for treating macular degeneration. The
CC present sequence represents a DNA encoding a human apolipoprotein E (Apo
CC E) (GenBank Accession No. K00396)
XX
SQ Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.13e-106 Length: 1156
Score: 1493.00 Matches: 299

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0
US-09-827-854A-2 (1-299) x ACC84919 (1-1156)
Qy 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
Db 115 AAGGTGAGCAGGCGGTGGAGACAGAGCCGAGGCCAGCTGCCAGCAGACCGAGTGG 174
Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTrpLeuArgTrpVal 40
Db 175 CAGAGCGCCAGCGCTGGAACTGGCACTGGGTGCTTTTGGATTACCTCGCTGGGTG 234
Qy 41 GlnThrLeuSerGluGlnValGlnGluGluLeuSerSerGlnValThrGlnGluLeu 60
Db 235 CAGACACTGTCTGAGCAGGTGCAGAGGAGGTGCTCAGCTCCAGGTCAACCAGAACTG 294
Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu 80
Db 295 AGGCGCTGATGGACGAGACCATGAGAGGATTGAAGGCTTACAAATCGGAACCTGGAG 354
Qy 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAla 100
Db 355 CAACTGACCCCGGTGGCGGAGGACGCGGCGACGGCTGTCCAAGGAGCTCAGCGCGG 414
Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 415 CAGGCCCGGTGGCGCGGACATGGAGGACGTGTGCGGCCCTGGTGCAGTACCGCGCGC 474
Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 475 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGAGCTGCGGGTGGCGCTCCCTCC 534
Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 535 CTGCGCAAGCTGCGTAAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAGCGCTGSCA 594
Qy 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
Db 595 GTGTACCAAGCGCGGCGCGCGAGGCGCGAGCGCGCTCAGCGCCATCCGCGAGCGC 654
Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 655 CTGGGGCCCTCTGTGGAAACAGGGCCGCTGCGGGCCGCCACTGTGGGCTCCTGCGCG 714
Qy 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
Db 715 CAGCCGCTACAGAGCGGCGGCCAGGCTGCGGGCGAGCGGCTGCGCGCGGATGAGAG 774
Qy 221 MetGlySerArgTrpArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 775 ATGGGACGCGGACCCCGCGACCGCTGTGGAGAGATGACGAGCCAGTGGCGCGGTGG 834
Qy 241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 835 GCCAAGCTGAGGAGCAGGCCCCAGCATAGCTGAGGCCGAGGCTTCCAGGCCGCGC 894
Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db 895 CTCGAAGAGCTGGTTTCGAGCCCTCGTGGAGACATGCAGGCCAGTGGCGCGGTGG 954
Qy 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 955 GAGAAGGTGCAGGCTGCGTGGGACCAGCGCCGCCCTGTGTGCCGAGCAATCAC 1011
RESULT 12
ADA14198
ID ADA14198 standard; cDNA; 1156 BP.
XX
AC ADA14198;
XX

DT 06-NOV-2003 (first entry)
 XX Human apolipoprotein E (ApoE) encoding cDNA SEQ ID NO:1.
 XX
 KW identification; fluorescence resonance energy transfer; FRET;
 KW single nucleotide polymorphism; SNP; mutation; nucleic acid polymerase;
 KW nucleic acid sequencing; human; apolipoprotein E; ApoE;
 KW chromosome 19q13.2; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 61..1014
 FT /*tag= a
 FT /product= "apolipoprotein E (ApoE) "
 XX
 PN WO2003068986-A1.
 XX
 XP 21-AUG-2003.
 XX
 XX 07-FEB-2003; 2003WO-BP050013.
 XX
 XX 11-FEB-2002; 2002EP-00100124.
 XX
 XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 XX
 XX Turcatti G;
 XX
 XX WPI; 2003-679643/64.
 XX P-PSDB; ADA14199.
 XX
 PT Identifying a nucleotide in a nucleic acid by means of Fluorescence
 PT Resonance Energy Transfer by monitoring the presence or absence of
 PT incorporation of the nucleotide chemically linked to the second FRET-
 PT generating fluorophore.
 XX
 PS Example 1; Page 50-51; 59pp; English.
 XX
 CC The present invention describes a method (M1) for identifying a
 CC nucleotide in a nucleic acid by means of fluorescence resonance energy
 CC transfer (FRET). M1 comprises: (a) providing a first nucleic acid
 CC containing the nucleotide to be identified in a single-stranded
 CC conformation at least in the portion including the nucleotide to be
 CC identified and the sequence immediately in 3' to the nucleotide; (b)
 CC providing a second nucleic acid comprising a single-stranded 3' end
 CC complementary to the sequence of the first nucleic acid immediately in 3'
 CC to the nucleotide to be identified, and a first FRET-generating
 CC fluorophore linked to a nucleotide located from 1-12 nucleotides far
 CC apart from the 3' terminal nucleotide of the second nucleic acid; (c)
 CC hybridising the first and second nucleic acid, resulting in a nucleic
 CC acid, where the sequence immediately in 3' to the nucleotide is in the
 CC double stranded conformation; (d) adding the nucleic acid polymerase and
 CC at least a nucleotide chemically linked to a second FRET-generating
 CC fluorophore; (e) allowing the nucleic acid polymerase to perform a single
 CC base extension at the 3' end of the first nucleic acid; and (f)
 CC monitoring the incorporation, or the absence of incorporation, of the
 CC nucleotide chemically linked to the second FRET-generating fluorophore
 CC using a FRET-based analytical technology. Also described: (1) identifying
 CC a single nucleotide polymorphism (SNP) or mutation; (2) evaluating the
 CC extension of properties of nucleic acid polymerases, or the preference of
 CC nucleic acid polymerases for the same nucleotide when labelled or non-
 CC labelled by employing M1; (3) screening modulators of nucleic acid
 CC polymerases by employing M1; (4) sequencing nucleic acids according to M1
 CC; and (5) kits, useful for the methods described above, comprising at
 CC least a nucleic acid having an internal nucleotide located from 1-12
 CC nucleotides far apart from the 3' terminal nucleotide linked to a first
 CC FRET-generating fluorophore polymerase and at least a nucleotide
 CC chemically linked to a second FRET-generating fluorophore. The methods
 CC and kits of the present invention are useful for identifying a SNP or
 CC mutation, evaluating the extension of properties of nucleic acid
 CC polymerases or the preference of nucleic acid polymerases for the same
 CC nucleotide when labelled or non-labelled, screening modulators of nucleic
 CC acid polymerases by employing the novel method, and sequencing nucleic

CC acids. The present sequence encodes human apolipoprotein E (ApoE), which
 CC is used in an example from the present invention. Human ApoE is located
 CC on chromosome 19q13.2.
 XX
 SQ Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 1.13e-106 Length: 1156
 Score: 1493.00 Matches: 299
 Percent Similarity: 100.0% Conservatives: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0
 US-09-827-854A-2 (1-299) x ADA14198 (1-1156)
 QY 1 LysValGluGlnAlaValGluThrGluProGluLeuArgGlnGlnThrGluTyr 20
 DB 115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCGAGCTGCGCCAGACAGACCGAGTGG 174
 QY 21 GlnSerGlyGlnArgTyrGluLeuAlaLeuGlyArgPheTyrAspTyrLeuArgTyrVal 40
 DB 175 CAGAGCGGCGAGCGCTGGGAACTGGCACTGGGTGGCTTTTGGATTACCTGGCTGGGTG 234
 QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
 DB 235 CAGACACTGTCTGAGCAGGTGAGGAGGAGCTGCTCAGCTCCAGGTCCAGGAACTG 294
 QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
 DB 295 AGGGCGCTGATGGACGAGACCATGAAGAGTTGAAGGCTTACAAATCGGAACTGGAGGAA 354
 QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
 DB 355 CAACTGACCCCGTGGCGGAGGAGACGCGGCGACGGCTGTCCAAGAGCTGCAAGCGCG 414
 QY 101 GlnAlaArgLeuGluAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
 DB 415 CAGGCGCGCTGGCGCGGACATGGAGGACGTGTGCGCGCGCTGTGTGTGATACCGCGCG 474
 QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
 DB 475 GAGGTGACAGCCCATGCTCGGCAGACAGACACGAGAGCTGCGGGTGGCGCTCGCTCCAC 534
 QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
 DB 535 CTGCGCAAGCTGCGTAAGCGGCTCTCTCGCGATGCGATGACCTGCAGAAGCGCTGGCA 594
 QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaAlaArgGluArg 180
 DB 595 GTGTACAGCG 654
 QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
 DB 655 CTGGGCGCGCTGGTGGAAACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 714
 QY 201 GlnProLeuGlnGluArgAlaGlnAlaTyrGlyGluArgLeuArgAlaArgMetGluGlu 220
 DB 715 CAGCGCTACAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 774
 QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
 DB 775 ATGGGCGAGCGGACCG 834
 QY 241 AlaLysLeuGluGluGlnAlaGlnGlnAlaArgLeuGlnAlaGluAlaPheGlnAlaArg 260
 DB 835 GCCAAGCTGGAGAGGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 894
 QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTyrAlaGlyLeuVal 280
 DB 895 CTCAGAGCTGGTTGAGCGCGCTGGTGGAAAGACATGCAAGCGCGCGCGCGCGCGCG 954
 QY 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299

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Db      955 GAGAAAGGTGCGCTGGCGACCGCCGCTGTGCTCCAGCGACAATCAC 1011
RESULT 13
ADP43409
ID      ADF43409 standard; DNA; 1156 BP.
AC
XX
AC      ADF43409;
XX
DT      12-FEB-2004 (first entry)
XX
DE      Apolipoprotein polynucleotide seqid 129.
XX
KW      receptor; lipid-based tumour associated antigen; cytostatic;
KW      antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW      infectious disease; apolipoprotein; ds.
XX
OS      Unidentified.
XX
XX      US2003157113-A1.
XX
XX      21-AUG-2003.
XX
XX      28-DEC-2000; 2000US-00751708.
XX
XX      28-DEC-1999; 99US-0173371P.
XX
XX      (TERM/) TERMAN D S.
XX
XX      Terman DS;
XX
XX      WPI; 2003-787326/74.
XX
XX      P-PSDB; ADF43410.
XX
XX      New receptor in a mammalian cell that inhibits regular activation by
PT      receptors specific for lipid-based tumor associated antigens, useful for
PT      treating a neoplastic disease or tumor, and infectious diseases.
XX
XX      Example 3; SEQ ID NO 129; 151pp; English.
XX
XX      The invention describes a receptor in a mammalian cell that inhibits
CC      regular activation by receptors specific for lipid-based tumour
CC      associated antigen. The receptor has cytostatic and antimicrobial
CC      properties and is suitable for use in gene therapy. The receptors,
CC      methods and compositions are useful for treating a neoplastic disease or
CC      tumour (cancer), and infectious diseases. This sequence represents
CC      apolipoprotein polynucleotide, a cell surface moiety, the DNA of which
CC      can be transfected into a cell with superantigen DNA to generate
CC      antitumour immunity.
XX
XX      Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.:      1.13e-106      Length:      1156
Score:          1493.00      Matches:      299
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:     100.0%      Indels:      0
DB:              10      Gaps:        0
US-09-827-854A-2 (1-299) x ADF43409 (1-1156)
Qy      1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnInThrGluTrp 20
Db      115 AAGGTGAGCAAGCGGTGGAGACAGACCGGAGCCGAGCTGCGCCAGCAGACCGAGTGG 174
Qy      21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db      175 CAGAGCGCCAGCGCTGGGAACTGGCACTGGGTGCTTTGGGATTTACCTGGCTGGGTG 234
Qy      41 GlnThrLeuSerGluGlnValGlnGluGluLeuSerSerGlnValThrGlnGluLeu 60
Db      235 CAGACACTGCTGAGCAGGTGCAGGAGGAGTGTCTAGTCTCCAGGTCAACCAGGAATCTG 294
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Qy      61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db      295 AGGGCGCTGATGGACGAGACCATGAAGGATTTGAAGGCTTCAAAATCGAACTGGAGGAA 354
Qy      81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db      355 CAACTGACCCCGGTGGCGGAGAGACGCGGCACGGCTGTCCAAGGAGCTGCAGCGCGCG 414
Qy      101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db      415 CAGGCCCGGTGGCGCGCGACATGAGAGACATGTGCGGCCCTGTGTGCTACGTACCGCGCG 474
Qy      121 GluValGlnAlaMetLeuGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db      475 GAGGTGCAGGCCCATGCTCGGCCAGAGACCCAGGAGTGCGGGTGCGCTCGCTCCAC 534
Qy      141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
Db      535 CTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATCCGATGACCTGCAGAACGCGCTGGCA 594
Qy      161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
Db      595 GTGTACCAAGCGCGGCGCGCGAGCGCGCGAGCGCGCTCAGCGCCATCCGAGCGCG 654
Qy      181 LeuGlyProLeuValGluGlnGlnValArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db      655 CTGGGGCCCCCTGTGTGGAAACAGGGCGCGGTGCGGGCCGCCACTGTGGGGCTCCTGCGCCGCG 714
Qy      201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
Db      715 CAGCCGCTACAGGAGCGGGCCAGCGCTGGGGCGAGCGGCTGCGCGCGGATGGAGGAG 774
Qy      221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db      775 ATGGGCGAGCGGACCGCGACCGCTGGACGAGGTGAAGGAGCAGGTGGCGGAGTGGCG 834
Qy      241 AlalysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db      835 GCCAAGCTGGAGGAGCAGGCGCCAGCATAGCTTCAGGCGCGAGGCTTCAGGCGCCGCG 894
Qy      261 LeuLysSerTrpPheGluProLeuValGluLysMetGlnArgGlnTrpAlaGlyLeuVal 280
Db      895 CTCAGAGCTGTTTCGAGCGCCCTGTGTGAAGACATGCAGCGCCAGTGGCGCGGGCTGGT 954
Qy      281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db      955 GAGAAGGTGACAGGCTGCGGTGGCCAGCGCCGCCCTGTGTGCCAGCGACAATCAC 1011
RESULT 14
AD131681
ID      AD131681 standard; cDNA; 1156 BP.
XX
AC      AD131681;
XX
DT      17-JUN-2004 (first entry)
XX
DE      Human cDNA #1007.
XX
KW      Human; gene; ss; immunological response; immunopathological condition;
KW      Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW      irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW      acute monocytic leukemia; antiinflammatory; antiasthmatic; antiulcer;
KW      osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS      Homo sapiens.
XX
XX      US6607879-B1.
XX
XX      19-AUG-2003.
XX
XX      09-FEB-1998; 98US-00023655.
XX
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PR 09-FEB-1998; 98US-00023655.
 XX (INCY-) INCYTE CORP.
 PA
 XX
 PI Cocks BG, Stuart SG, Seilhamer JJ;
 XX
 DR WPI; 2003-895307/82.
 XX
 PT A composition comprising a plurality of cDNAs, useful for detecting
 PT altered expression of genes in an immunological response or for
 PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
 PT or osteoarthritis.
 XX
 XX Claim 1; SEQ ID NO 1007; 50pp; English.
 XX
 CC The invention relates to a composition comprising a plurality of cDNAs
 CC for detecting the altered expression of genes in an immunological
 CC response. The invention also relates to a method of diagnosing or
 CC monitoring the treatment of an immunopathological condition in a sample,
 CC comprising obtaining nucleic acids from a sample, contacting the nucleic
 CC acids of the sample with an array comprising the plurality of cDNAs under
 CC conditions to form one or more hybridisation complexes, detecting the
 CC hybridisation complexes and comparing the levels of the detected
 CC hybridisation complexes with the level of hybridisation complexes
 CC detected in a non-diseased sample, where an altered level of the detected
 CC hybridisation complexes correlates with the presence of an
 CC immunopathological condition. Also disclosed are an expression profile
 CC comprising a microarray and a plurality of detectable complexes and a
 CC method for identifying a plurality of polynucleotide probes. The cDNAs
 CC are useful as hybridisable array elements in a microarray for monitoring
 CC the expression of target polynucleotides. The microarray can be used in
 CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
 CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
 CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
 CC identifying agents for the treatment of the diseases. The microarray may
 CC also be used in drug discovery and development, toxicological and
 CC carcinogenicity studies, forensics or pharmacogenomics. The composition
 CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
 CC genomic fragments. This sequence represents a human cDNA of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification but was obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.13e-106 Length: 1156
 Score: 1493.00 Matches: 299
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 11 Gaps: 0
 US-09-827-854A-2 (1-299) x AD131681 (1-1156)
 QY 1 LysValGluGlnAlaValGluThrGluProGluLeuArgGlnThrGluTrp 20
 Db 115 AAGGTGAGCAAGCGGTGGAGACAGAGCCGAGCGCGAGTGGCCAGCAGACCGAGTGG 174
 QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
 Db 175 CAGAGCGCGCAGCGCTGGCACTGGCTCGCTCTTTGGGATTACCTGCGCTGGGTG 234
 QY 41 GlnThrLeuSerGluGlnValGlnGlnGluLeuSerSerGlnValThrGlnGluLeu 60
 Db 235 CAGACACTGTCTAGCAGGTGACGAGAGAGCTGCTCAGCTCCAGGTTCACCCAGGAACCTG 294
 QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
 Db 295 AGGCGCTGATGGACGAGACCCATGAAGAGTTGAAGGCCTACAAATCGGAACCTGAGGAA 354
 QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100

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 AC AEB86465;
 XX
 DT 06-OCT-2005 (first entry)
 XX
 DE Human apolipoprotein E encoding DNA.
 XX
 KW selectable marker; osteopathic; antiarthritic; diagnosis; osteoarthritis;
 KW cartilage damage; fractures; gene; ds; apolipoprotein E.
 XX
 OS Homo sapiens.
 XX
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 XX
 PD 12-AUG-2003.
 XX
 PF 29-NOV-2002; 2002JP-00348073.
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 PR 30-NOV-2001; 2001JP-00367993.
 XX
 PA (SUMU) SUMITOMO SEIYAKU KK.
 XX
 DR WPI; 2003-703023/67.

DR P-PSDB; AEB86466.
 XX Marker for screening for compounds influencing a gene or protein, for
 PT treating cartilage disorders, such as, osteoarthritis, comprises a
 PT polynucleotide or a complement to specific genes, or an antibody to its
 XX protein.
 XX
 PS Claim 1; SEQ ID NO 13; 64pp; Japanese.
 XX
 CC The invention relates to a novel marker for cartilage disorders. The
 CC marker consists of a polynucleotide sequence of 15 bases from the
 CC sequence of acetyl-Coenzyme A acetyltransferase 1, Rev-Erba-beta,
 CC Selenoprotein P, aquaporin 1, BMP-3b; FK506-binding protein 1A,
 CC apolipoprotein E, acyl-CoA synthetase 5, epoxide hydrolase 1, or
 CC glutamine synthase gene, and/or a polynucleotide complementary to one of
 CC these. The invention further comprises: a detection method of a cartilage
 CC disorder; a disease marker for cartilage disease containing an antibody
 CC to the amino acid, as given in the specification; a detection method of a
 CC cartilage disorder using a protein sample from the subject, or a peptide
 CC from it, and the antibody as a label; screening for a material which
 CC controls expression of one of the genes above; screening for a material
 CC which controls the activity or function of one of the proteins; and an
 CC agent to improve or treat a cartilage disorder which contains a substance
 CC controlling expression of the genes or activity of the proteins. The
 CC novel marker has osteopathic and antiarthritic activities. The markers
 CC may be used as a probe or a primer, for diagnosis of conditions such as
 CC osteoarthritis, chondrodystrophy, discopathy, cartilage damage, semilunar
 CC cartilage disorder, deficient healing of fractures, or in chondrocyte
 CC transplants. The screening methods are useful for identifying therapeutic
 CC compounds. This polynucleotide sequence represents the DNA encoding
 CC apolipoprotein E of the invention.
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 SQ Sequence 1156 BP; 208 A; 368 C; 432 G; 148 T; 0 U; 0 Other;

Alignment Scores:

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Score:	1493.00	Matches:	299
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US-09-827-854A-2 (1-299) x AEB86465 (1-1156)

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Qy	41	GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu	60
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Qy	61	ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu	80
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Db	475	GAGGTGAGGCGCATGCTCGGCCAGAGCAGCAGGAGGTGCGGGTGCCTGCCCTCCAC	534
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Qy	221	MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg	240
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Qy	281	GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis	299
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 Job time : 1035.05 secs

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GenCore version 5.1.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 19:02:39 ; Search time 7915.48 Seconds
(without alignments)
3168.451 Million cell updates/sec

Title: US-09-827-854A-2

Perfect score: 1493

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Scoring table: BLOSUM62

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1162	77.8	842	2	BG763371 602735433

5	1156	77.4	933	2	B1668318
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ALIGNMENTS

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ILLUMIGEN MCQ 48393 Katze MMLV Macaca mulatta cDNA clone
IBIUW:18409 57 similar to Bases 755 to 975 highly similar to human
Unigene Hs.515465, mRNA sequence.

ACCESSION C0580643
VERSION C0580643.1 GI:50411831
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)

ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 975)
AUTHORS Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.

TITLE Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human

JOURNAL Genome Biol. 6 (7), R60 (2005)
PUBMED 15998449
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com

Sequenced on 2004.07.02. 690 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see <http://www.macaque.org>

PCR Primers
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US-09-827-854a-2 (1-299) x COS80643 (1-975)

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RESULT 2

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 ILLUMIGEN MCQ 52207 Katze MNLV Macaca nemestrina cDNA clone
 IBIUM:28954 57 similar to Bases 5 to 934 highly similar to human
 APOE (Hs.110675), mRNA sequence.
 CO775017
 VERSION 1
 KEYWORDS
 SOURCE
 ORGANISM
 Macaca nemestrina (pig-tailed macaque)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopitheidae; Cercopithecinae; Macaca.
 REFERENCE
 AUTHORS
 Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
 Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
 Tadonato,S.P.
 Analysis of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 Genome Biol. 6 (7), R60 (2005)
 1599849
 COMMENT
 Contact: C. Magness
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2004.07.21. 706 Q20 bases. Library Preparation: Prof.
 Michael Katze Lab at University of Washington DNA Sequencing:
 Illumigen Biosciences Inc. For further information, see
<http://www.macaque.org>
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FEATURES

source

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ORIGIN

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Query Match: 81.0% Indels: 1
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US-09-827-854A-2 (1-299) x CO775017 (1-937)

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Qy 260 gLeuLysSerTrpPheGluProLeuValGluAspMetClnArgGlnTrpAlaGlyLeuVa 280
Db 864 CCCCCAAAACCTGGTTCAGGCCCCCTGGTGGAAAAAATGGACCGCGCGGGGCTGGCTGG 923
Qy 280 lGluLys 282
|||||

Db 924 TGA AAAA 930

RESULT 3

Bi670367

LOCUS

DEFINITION 603292738F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312024 5',
mRNA sequence.

ACCESSION

VERSION Bi670367.1 GI:15584600

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 1027)

TITLE NIH-MGC http://mgs.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: csapbs-x@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LHAM1790 row: 1 column: 09

High quality sequence stop: 845.

FEATURES

source

1..1027
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5312024"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to 5. This is a
primary library enriched for full-length clones and
constructed using the cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NHGRI/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 2.06e-104 Length: 1027
Score: 1198.50 Matches: 274
Percent Similarity: 90.3% Conservative: 6
Best Local Similarity: 88.4% Mismatches: 19
Query Match: 80.3% Indels: 12
DB: 2 Gaps: 2

US-09-827-854A-2 (1-299) x Bi670367 (1-1027)

Qy 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
Db 80 AAGGTGAGCAACCGGTGGAGACAGACCGGAGCGCGAGTTCGCCAGCGAGTGG 139
Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 140 CAGAGCGCCAGCGCTGGGAACTGGCACTGGCTGGCTGGCTGGCTGGCTGGCTGG 199
Qy 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 200 CAGACACTGTCTGAGCAGGTGCAGAGAGCTGCTCAGCTCCAGGTCACCCAGCAACTG 259

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QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu 80
Db 260 AGGGCGCTGATGACGAGACCATGAAGGAGTTGAAGGCGCTTACAAATCGGAACCTGGAGGAA 319
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAla 100
Db 320 CAACTACCCCGCTGGCGGAGAGACCGCGGACGCTGTCAAAGGAGCTGCAAGCGCGG 379
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyValArgLeuValGlnTyrArgGly 120
Db 380 CAGGCCCGCTGGCGCGGACATGGAGGAGCTGTGGCGCGCTGTGTGAGTACGACCGCGG 439
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 440 GAGGTGCAGGCCATGCTCGGCCAGAGACCGAGGAGCTGCGGTGCGCTCGCTCCAC 499
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 500 CTCGCAAGCTGGTAAAGCGCTCTCCGCGATGCCGATGACCTGCAGAGCGCTGGCA 559
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
Db 560 GTGTACAGCCCGGGGCCCGAGGCGCGCGGCTCAGCCCATCCCGAGCGC 619
QY 181 Leu-GlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaG 200
Db 620 CTGGGGCCCCCTGTTGGACAGGTCCCGTGTGGCGCGCCACTGTGGGTCTCCCTGGCCGG 679
QY 200 yGlnProLeuGlnGluArgAlaGlnAlaThrGlyGluArg-LeuArgAlaArgMetGluG 220
Db 680 CCAGCCCGCTACAGAGCGGGCCAAAGCGCTGGGCGGAGCGGCTTGGCGCGCGATGGAGG 739
QY 220 lu-MetGlySerArg-ThrArgAspArgLeuAspGluValLysGluGlnValAlaGlu-V 239
Db 740 AAGAGGGGCGAGCGGAGCCCGACCGCTGGACCGAGGTGAGGAGCAGGTGGCGGAGG 799
QY 239 aArgAlaLysLeu---GluGluGlnAlaGlnGln-IleArgLeuGln-AlaGluAlaPh 257
Db 800 TGGCGGCCCAAGCTGGAGCGGAGCGAGCCCGAGCAAGATACGCTGCAGGCGCGAGGCTTC 859
QY 257 eGlnAlaArgLeuLysSerTrpPheGluPro-----LeuValGluAspMetGlnArgG 275
Db 860 CTAGGCGCGCGCTCAGAGCTGGTTCGAACCCCTGGGTGGAAACGACATGGCGCGGCCCA 919
QY 275 nTTPAlaGlyLeuValGluLysVal-GlnAlaAlaValGlyThrSerAlaAlaProValP 295
Db 920 GTGGCGCGCTGGTGGAAAGGTGTCAGGCTGCGGGGGCACACCGCGCGCTGTGTGTC 979
QY 295 roSerAspAsnHis 299
Db 980 CAGC-GACAATCAT 992
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RESULT 4
BG763371
LOCUS 602735433F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4860585 5',
DEFINITION mRNA sequence.
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ACCESSION BG763371
VERSION BG763371.1 GI:14074024
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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```
REFERENCE 1 (bases 1 to 842)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTP/DTP
```

cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM1718 row: b column: 10
High quality sequence stop: 817.
Location/Qualifiers

FEATURES

source
1..842
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4860585"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 43"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. |"

ORIGIN

Alignment Scores:
Pred. No.: 5,06e-101 Length: 842
Score: 1162.00 Matches: 242
Percent Similarity: 96.8% Conservative: 2
Best Local Similarity: 96.0% Mismatches: 7
Query Match: 77.8% Indels: 2
DB: 2 Gaps: 0
US-09-827-854A-2 (1-299) x BG763371 (1-842)
QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
Db 90 AAGGTGAGCAAGCGTGGAGCAGAGCCGAGCGCGAGCTGCGCCAGCAGACCGAGTGG 149
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 150 CAGAGCGCGCAGCGCTGGGAACCTGGCACTGGGTCTGTTGGATTTACCTGCGCTGGGTG 209
QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 210 CAGACACTGTCTGAGCAGGTGCGAGGAGAGCTGCTCAGCTCCAGGTCACCCAGGAACTG 269
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 270 AGGGCGCTGATGACGAGACCATGAAGGAGTTGAAGGCGCTTACAAATCGGAACCTGGAGGAA 329
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db 330 CAACTACCCCGCTGGCGGAGAGACCGCGGACGCTGTCAAAGGAGCTGCAAGCGCGG 389
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyValArgLeuValGlnTyrArgGly 120
Db 390 CAGGCCCGCTGGCGCGGACATGGAGGAGCTGTGGCGCGCTGTGTGAGTACGACCGCGG 449
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 450 GAGGTGCAGGCCATGCTCGGCCAGAGACCGAGGAGCTGCGGTGCGCTCGCTCCAC 509
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 510 CTCGCAAGCTGGTAAAGCGCTCTCCGCGATGCCGATGACCTGCAGAGCGCTGGCA 569
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
Db 570 GTGTACAGCCCGGGGCCCGAGGCGCGCGGCTCAGCGCGCTCAGCGCCATCCCGAGCGC 629

QY 181 LeuGlyProLeuValGluGlnGlyValArgAlaAlaThrValGlySerLeuAlaGly 200
 |||||
 Db 630 CTGGGGCCCTG-GTGGAAACAGGGCCGGTGGCGGCGCGAACTGTGGCTCTCTGGCCGCG 688
 QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuAlaArgMetGluGlu 220
 |||||
 Db 689 CAGCCGCTACAGGAGCGGGCCAGCGCTGGGGCGAGCGGCTGCGCGCGGATGGAGAG 748
 QY 221 Met-GlySerArgThrArgAspArgLeuAspGluValIysGluGlnValAlaGluValAr 240
 |||||
 Db 749 ATGCGGAGCGGCGGACCCGCGACCGCTGGAGAGGTGAAGGACGACGAGTGGCGGAGTGGC 808
 QY 240 gAlaLysLeuGluGlnAlaGlnGlnIleArg 251
 |||||
 Db 809 CGCAAGCTGGGAGGAGCAGGCCACGACGATACGC 842

RESULT 5

BI668318 933 bp mRNA linear EST 12-SEP-2001
 LOCUS 603295681F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5314844 5',
 DEFINITION mRNA sequence.

ACCESSION BI668318.1 GI:15582551

VERSION EST.
 KEYWORDS Homo sapiens (human)

SOURCE
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.

AUTHORS

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM1798 row: a column: 21

High quality sequence stop: 780.

Location/Qualifiers

1. .933

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5314844"

/tissue_type="hypothalamus"

/lab_host="DH10B"

/clone_lib="NIH MGC 96"

/note="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI

(Gcgag); Oligo-dr primed using primer

5'-TTTTTTTTTTTTTNN-3', size-selected for average

insert size 2.3 kb and normalized to ROT 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein,

(NIH/NHGRI, National Institutes of Health). Note: this is

a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 2,17e-100 Length: 933
 Score: 1156.00 Matches: 245
 Percent Similarity: 93.7% Conservative: 7
 Best Local Similarity: 91.1% Mismatches: 14
 Query Match: 77.4% Indels: 4

Db: 2 Gaps: 1
 US-09-827-854A-2 (1-299) x BI668318 (1-933)
 QY 1 LysValGluGlnAlaValGluThrGluProGluLeuArgGlnGlnThrGluTrp 20
 |||||
 Db 129 AAGGTGGAAGCAAGCGGTGGAGACAGAGCCGGAGCCGAGCTGCGCCAGACAGACCGAGTGG 188
 QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyValArgPheTrpAspTyrLeuArgTrpVal 40
 |||||
 Db 189 CAGAGCGCCAGCCGCTGGCACTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 248
 QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
 |||||
 Db 249 CAGACACTGTCTGAGCAGAGTGCAGGAGGAGTGTCTAGCTCCCAAGTCAACCCAGGAACTG 308
 QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
 |||||
 Db 309 AGGCGCGTGTATGGACGAGACCATGAAGAGTGTGAAGGCCTACAAATCGGAACCTGGAGAA 368
 QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
 |||||
 Db 369 CAACTGACCCCGGTGGCGGAGGAGACGCGGCGACGGCTGTCCAAGGAGCTCGACGCGCGC 428
 QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
 |||||
 Db 429 CAGGCCCGCTGGCGCGCGACATGGAGGACGTGTGCGCGCCGCTGTGTGCTGCTGCTGCTGCTG 488
 QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
 |||||
 Db 489 GAGGTGCAGGCCATGCTCGGCCAGACGACGAGGAGTGGCGGTGCGCTGCTGCTGCTGCTGCTG 548
 QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
 |||||
 Db 549 CTGCGCAAGCTGGCTAAGCGGCTCTCCCGGATCCCATGACCTGCGAGAGCGCTGCGAGAGCG 608
 QY 161 ValTyrGlnAlaGlyAlaArgGluGluValAlaGluArgGlyLeuSerAlaIleArgGluArg 180
 |||||
 Db 609 GTGTACAGCGCGGGGCGCGGAGGCGCGGAGCGCGCTCAGCGCCATCCGCGAGCGC 668
 QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
 |||||
 Db 669 CTGGGGCCCTGTGTGGAACAGGCGCGTGGCGGCGCGCTGTGTGGCTGCTGCTGCTGCTGCTG 728
 QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyValArgLeuArgAlaArg-MetGlu-- 219
 |||||
 Db 729 CAGCCGCTACAGGAGCGGCGCGGCGCTGGCGGCGGCGCTGCGCGCGGAGATTGGAGGC 788
 QY 220 -GluMetGlySerArgThrArgAspArgLeuAsp-GluValLysGluGlnValAlaGluV 239
 |||||
 Db 789 ACATTGGGGCAGCGGACCCCGGACCGCTGGAAACGAGGTGAAGGAGCGGTGCGGAAGT 848
 QY 239 alArgAlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnA 259
 |||||
 Db 849 TGGCGCCCAAGAGCTGGGGGACCAAGGCCCGCAATTCGCTTTCGAGGCCAA-SCCTTCCAGG 907
 QY 259 laArgLeuLysSerTrpPheGlu 266
 |||||
 Db 908 CCGGCTCCAAGAGCTGTTCAA 930
 RESULT 6
 CX165559 786 bp mRNA linear EST 23-DEC-2004
 LOCUS HESC2_30_A09.g1_A035 NIH_MGC_258 Homo sapiens cDNA clone
 DEFINITION IMAGE:7469084 5', mRNA sequence.
 ACCESSION CX165559
 VERSION CX165559.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

```

REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: BreaGen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM15769 row: a column: 18
Seq primer: JENREV (CAGGAACAGCTATGACC)
High quality sequence stop: 786.

FEATURES
source
1..786
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7469084"
/sex="male"
/tissue_type="human embryonic stem cells differentiated to
an early endodermal cell type"
/cell_type="human embryonic stem cells"
/cell_line="BG01"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH MGC 258"
/notes="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early endodermal cell type. Cell line
id and NIH Registry designation is BG01. Positive for
GATA4, Mx1, HNF4alpha expression; negative for AFP
expression. Passage number 40. cDNA primed using oligo-dT
primers: 5'-pGACTAGTCTAGATCGGCGGCCCT(T)25-3' and
cloned into the EcoRV/NotI sites of pExpress-1. This
primary library is non-normalized (normalized primary
library is NIH MGC 259). It was constructed by Express
Genomics (Frederick, MD). Sequence ends have been trimmed
to exclude vector and regions below phred quality 16.
Three-prime sequences are presented as their reverse
complement and have been trimmed to exclude polyA. Note:
this is a Mammalian Gene Collection library."

ORIGIN
Alignment Scores:
Pred. No.: 3,84e-99 Length: 786
Score: 1142.00 Matches: 229
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.5% Indels: 0
DB: 8 Gaps: 0

US-09-827-854A-2 (1-299) x CX165559 (1-786)

QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnThrGluTrp 20
Db 100 AAGGTGGAGCAAGCGGTGGAGACAGAGCGGAGCGGAGCTGCGCCAGCAGACCGAGTGG 159
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTrpVal 40
Db 160 CAGAGCGCGCAGCGCTGGCACTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 219
QY 41 GlnThrLeuSerGluGlnValGlnGlnGluLeuSerSerGlnValThrGlnGluLeu 60
Db 220 CAGACACTGTGTGAGCAGAGGTGCAGGAGGAGCTGTCTAGCTCCCGAGTCAACCCAGGAAG 279

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QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu 80
Db 280 AGGGCGCTGATGCAGCAGACCATGAGGAGTTGAAGGGCTTCAAAATCGGAACCTGGAGGA 339
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAla 100
Db 340 CAACTGACCCCGTGGCGAGGAGACGCGGCGCGCTGTCCAGGAGCTGCAGGCGCGG 399
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 400 CAGGCGCGCTGGCGCGGACATGAGGACGTGTGCGCGCGCTGGTGCAGTACCGCGGC 459
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 460 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGGCGCTCCCTCCCAC 519
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 520 CTGCGCAGCTGCGTAAGCGCTCTCCGCGATGCGATGACCTGCAGAGAGCGCTGGCA 579
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLysSerAlaLeuArgGluArg 180
Db 580 GTGTACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCTCAGCGCCATCCGCGAGCGC 639
QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 640 CTGGCGCGCTGGTGGTAAACAGGCGCGCTGCGCGCGCGCGCTGTGGGCTCCCTGGCGCGC 699
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
Db 700 CAGCGCTACAGAGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGCGCGCGCTGGCGCGGAG 759
QY 221 MetGlySerArgThrArgAspArgLeu 229
Db 760 ATGGCAGCGCGCGCGCGCGCGCGCGCGCGCGCTG 786

RESULT 7
BU849868
LOCUS AGENCOURT 10440638 NIH MGC 109 Homo sapiens linear EST 16-OCT-2002
IMAGE:6598569 5', mRNA_sequence.
DEFINITION BU849868.1 GI:24034831
ACCESSION BU849868
VERSION BU849868.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 909)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM2831 row: j column: 09
High quality sequence stop: 574.

FEATURES
source
1..909
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6598569"
/tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_109"

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/note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 1.25e-98 Length: 909
 Score: 1137.50 Matches: 242
 Percent Similarity: 90.8% Conservatives: 6
 Best Local Similarity: 88.6% Mismatches: 19
 Query Match: 76.2% Indels: 6
 DB: 3 Gaps: 1

US-09-827-854A-2 (1-299) x BU849868 (1-909)

QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
 DB 95 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCGAGCTGCCCGCAGCAGACCGAGTGG 154
 QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
 DB 155 CAGAGCGCCAGCGCTGGGAACCTGGCACTGGCTCGCTTTGGGATTACCTGGCTGGGTG 214
 QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
 DB 215 CAGACACTGTCTGAGCAGGTGCAGAGAGAGCTGCTCAGCTCCAGGTCACCCAGGAAC 274
 QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
 DB 275 AGGCGCTGATGGACAGACCATGAGAGGTTGAAGGCCTACAANTCGAACTGGAGAA 334
 QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
 DB 335 CAACGTACCCCGGTGGCGGAGGACGCGGCACGGCTGTCCAAGGAGCTGCAGCGCGG 394
 QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
 DB 395 CAGCGCCGCTGGCGCGGACATGGAGAGCGTGTGCGCGCCCTCGGTGTCAGTACCGCGC 454
 QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
 DB 455 GAGGTGAGGCCATGCTCGGCCAGAGCACCGAGAGCTGCGGGTGCCTCGCTCCAC 514
 QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
 DB 515 CTGCGCAAGCTGCTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAGCGCTGGCA 574
 QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaAlaArgGluArg 180
 DB 575 GTGTACAGCGCGCGGCGCGAGCGCGCGGCTCAGCGCATCCCGCAGCGC 634
 QY 181 Leu-GlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaG 200
 DB 635 CTGGGGGCGCCCTGTGTGAACAGGGCGCGTGCAGGCGCGCCACTGTGGCTCCCTGGGCGG 694
 QY 200 YGlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuAlaArg---MetG 219
 DB 695 CCAGCCGCTACAGAGCGGGGCCAGGCTTGGGGCGAGCGGCTGCCCGCGGGATGGA 754
 QY 219 uGluMetGlySerArg-ThrArgAspArgLeuAspGluValLysGluGlnValAlaGlu- 238
 DB 755 AGAGATGGCAACCGGAACCCCGCACCGCTTGGAAAGGTGAAGGACCGAGTGGCGGAAG 814
 QY 239 -ValArgAlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaPheG 258
 DB 815 GTGCCCCCGAGCTGGAGGAAGCAGGCCACAAAACGCTGCAGGCGCGAGGCTTCCA 874
 QY 258 n-AlaArgLeuLysSerTrpPheGluPro 267

Db 875 GGGCCCGCTTCAAGAACTGGTTCAGGCC 903
 RESULT 8
 EG761746
 LOCUS
 DEFINITION 602717942F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4841411 5', mRNA sequence.
 ACCESSION BG761746
 VERSION BG761746.1 GI:14072399
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 938)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Plate: LICM1674 row: c column: 12
 High quality sequence stop: 767.
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 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4841411"
 /tissue_type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_49"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"

ORIGIN

Alignment Scores:
 Pred. No.: 1.06e-97 Length: 938
 Score: 1128.00 Matches: 254
 Percent Similarity: 92.1% Conservatives: 4
 Best Local Similarity: 90.7% Mismatches: 11
 Query Match: 75.6% Indels: 11
 DB: 2 Gaps: 2

US-09-827-854A-2 (1-299) x BG761746 (1-938)

QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
 DB 111 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCGAGCTGCCCGCAGCAGACCGAGTGG 170
 QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
 DB 171 CAGAGCGCCAGCGCTGGGAACCTGGCACTGGCTCGCTTTGGGATTACCTGGCTGGGTG 230
 QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
 DB 231 CAGACACTGTCTGAGCAGGTGCAGAGAGAGCTGCTCAGCTCCCGAGGTCACCCAGGAAC 290

FEATURES		Location/Qualifiers	
source		1. .942	
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		/clone="IMAGE:5301010"	
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		/lab_host="DH10B"	
		/clone_lib="NIH_MGC_96"	
		/note="Organ: brain; Vector: pBluescriptR (modified	
		pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI	
		(gtcag); Oligo-dT primed using primer	
		5'-TTTTTTTTTTTNN-3', size-selected for average	
		insert size 2.3 kb and normalized to R0T 5. This is a	
		primary library enriched for full-length clones and	
		constructed using the Cap-trapper method (Carninci,	
		preparation). Library constructed by M. Brownstein	
		(NIH/NHGRI, National Institutes of Health). Note: this is	
		a NIH_MGC Library."	
ORIGIN			
Alignment Scores:		Length: 942	
Pred. No.:		1,85e-97	
Score:		1125.50	
Percent Similarity:		93.0%	
Best Local Similarity:		90.8%	
Query Match:		75.4%	
DB:		2	
US-09-827-854A-2 (1-299) x BI600906 (1-942)			
Qy	1	LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp	20
Db	127	AAGGTGGAGCAAGCGGTGGAGACAGAGCCGAGCTGCGCCAGCAGACCGAGTGG	186
Qy	21	GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal	40
Db	187	CAGAGCGCCGAGCGCTGGGAACCTGGCTCTTTGGATTACCTGCGCTGGGTG	246
Qy	41	GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu	60
Db	247	CAGACACTGTCTGAGCAGGTGCGAGGAGCTGCTCAGCTCCAGGTCCACAGGAATG	306
Qy	61	ArgAlaLeuMetAspGluThrMethyGluLeuLeuAlaTyrIysSerGluLeuGluGlu	80
Db	307	AGGCGCTGATGACGAGACCATGAAGAGTGAAGGCCCTACAAATCGGAATCGAGGAA	366
Qy	81	GlnLeuThrProValAlaGluThrArgAlaArgLeuSerIysGluLeuGlnAlaAla	100
Db	367	CAACTGACCCCGTGGCGGAGAGACGCGGCGACGCTGTCCAAGGAGCTGCAGCGCGC	426
Qy	101	GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly	120
Db	427	CAGCGCGCTGGCGGCGGACATGGAGAGCTGTGCGCGCCCTGTGTGCTGCTACCGCGC	486
Qy	121	GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis	140
Db	487	GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGAGCTGCGGTGCGCTCGCTCCAC	546
Qy	141	LeuArgIysLeuArgIysArgLeuLeuArgAspAlaAspAspLeuGlnIysArgLeuAla	160
Db	547	CTGCGCAAGCTGGCTAAGCGGCTCTCCCGCGATGCCGATGACCTGCAGAGCGCTGCCA	606
Qy	161	ValTyrGlnAlaGlyAlaArgGluGluValAlaGluArgGlyLeuSerAlaLeuArgGluArg	180
Db	607	GTGTACAGCGCGGCGCCCGGAGGCGCGGAGCGGCGCTCAGCGCCATCCCGAGCGC	666
Qy	181	LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly	200
Db	667	CTGGGGCCCTGTGTGGAACAGGCGCGTGCAGGAGTGCAGTGTGGGCTCCCTGCGCGC	725
Qy	201	GlnProLeuGlnGluArgAlaGlnAlaTrpGluArgLeuArgAla-ArgMetGlu-G	220
61 ArgAlaLeuMetAspGluThrMethyGluLeuLeuAlaTyrIysSerGluLeuGluGlu		80	
291 AGGCGCTGATGACGAGACCATGAAGAGTGAAGGCCCTACAAATCGGAATCGAGGAA		350	
81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerIysGluLeuGlnAlaAla		100	
351 CAACTGACCCCGTGGCGGAGAGACGCGGCAAGCTGTCCAAGAGAGTGCAGGCGCGC		410	
101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly		120	
411 CAGCGCGCTGGCGGCGGACATGGAGAGCTGTGCGCGCCCTGTGTGCTGCTACCGCGC		470	
121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis		140	
471 GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGAGCTGCGGTGCGCTCGCTCCAC		530	
141 LeuArgIysLeuArgIysArgLeuLeuArgAspAlaAspAspLeuGlnIysArgLeuAla		160	
531 CTGCGCAAGCTGGCTAAGCGGCTCTCCCGCGATGCCGATGACCTGCAGAGCGCTGGCA		590	
161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaLeuArgGluArg		180	
591 GTGTACAGCGCGGCGCCCGGAGGCGCGGAGCGCTGCTCAGCGCCATCCCGAGCGC		650	
181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySer-LeuAlaG		200	
651 CTGGGGCCCTGTGTGGAACAGGCGCGCTGCGGCGCGCACTGTGGCTCCCTTGGCGCG		710	
200 yGlnProLeuGlnGluArgAlaGlnAlaTrp-GlyGluArg-LeuArgAlaArgMetGlu		219	
711 CCAGCGCTACAGAGCGGCGCCAGCGCTGGGCGGAGCGGCTTGGCGCGCGGATGGAG		770	
220 ---GluMetGlySerArgThr-Arg-AspArgLeuAspGluValIys-GluGlnValAla		237	
771 GGCATTTGGCGACCCCGACCCCGCGACCGCTTGGACGAGGTGAAGGAGCGAGTGGCG		830	
238 ---GluValArgAlaIysLeuGluGlu-GlnAlaGlnGlnIleArgLeuGlnAla---Glu		255	
831 GGAAGGTTGGCGCCCAAGCTGGAGGAAGCAGGCGCGAGGATACGCTGCGAGCGCGAAG		890	
256 AlaPheGlnAlaArgLeuIysSerTrpPheGluProLeuVal		269	
891 GGCTTCCAGCGCGGCTCAAAAGCTGGTTCGAAGCCCTGGTT		932	
BI600906		942 bp mRNA linear EST 07-SEP-2001	
603249241P1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5301010 5',		mRNA sequence.	
BI600906			
BI600906.1 GI:15493845			
EST.			
Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo.			
1 (bases 1 to 942)			
NIH-MGC http://mgs.nci.nih.gov/ .			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs-r@mail.nih.gov			
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.			
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki			
Toshlyuki and Piero Carninci (RIKEN)			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Incyte Genomics, Inc.			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
Plate: LLNL1762 row: a column: 11			
High quality sequence stop: 762.			

Db 726 CAGCCGCTACAGGAGCGGCGCCAGGCGCTGGGGCGAGCGGGTGGCGCGCGATGGAGGC 785

Qy 220 luMetGlySerArgThrArgAspArgLeuAap-GluValLys-GluGlnValAlaGluVa 239

Db 786 AGATTGGACGCGGACCGACCGGCTGGACCGAGGTGAACGACGAGGTTCGCGAAGT 845

Qy 239 l-ArgAlaLysLeuGluGlnAla---GlnGlnIleArgLeuGlnAlaGluAlaPheG 258

Db 846 TGGCGGCCAACTTGGAGGACACGCGCCAGCAGATACGCCTTGCAGGCGGAGGCCCTTC 905

Qy 258 lnAlaArgLeuLysSerTrpPheGluPro 267

Db 906 AGGCCGCGCTCAAAAC-TGGTTGACCCCT 933

RESULT 10

BM042676/c
LOCUS 603616028T1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420598 3',
DEFINITION mRNA sequence.

ACCESSION BM042676

VERSION BM042676.1 GI:16771943

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

1 (bases 1 to 834)

NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaaps-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM1875 row: h column: 07

High quality sequence start: 23

High quality sequence stop: 834.

FEATURES

source

1..834

location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

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/clones="IMAGE:5420598"

/tissue_type="melanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_112"

/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCACGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

ORIGIN

Alignment Scores: 2.75e-97 Length: 834

Pred. No.: 1123.00 Matches: 241

Score: 97.2% Conservative: 2

Percent Similarity: 96.4% Mismatches: 1

Best Local Similarity: 75.2% Indels: 6

Query Match: 2 Gaps: 0

DB:

US-09-827-854a-2 (1-299) x BM042676 (1-834)

Qy 56 ValThrGlnGluLeuAlaLeuMetAspGluThrMet--LysGluLeuLysAlaTyrL 75

Db 833 GTCAACCAGCAACTGAGGCGCTGATGAGCGAGACCATGGAAGGAGCGTTGAAGCGGTACA 774

Qy 75 ySerGluLeuGlu-GluGln-LeuThrProValAlaGluGluThrArgAlaArgLeuSe 94

Db 773 AATCGGAACCTGGAGGGAACAACCTGACCCCGTGGCGAGGAAACGCGGCGACGCTGTC 714

Qy 94 rLysGlu-LeuGlnAlaGlnAlaArgLeuGlyAlaAspMetGluAspValCysGly 113

Db 713 CAAGGACGCTTGCAGGCGGCGCAGCCGCTGGCGCGGACATGGAGGAGCTGTGCGCGC 654

Qy 114 ArgLeuValGlnTyrArgGlyGluValGlnAlaMetLeuGlyGlnSerThrGluGluLeu 133

Db 653 CGCCTGGTGCAGTACCGCGCGAGGTGCAGGCCCATGCTCGGCCAGAGCAGCCGAGGCTG 594

Qy 134 ArgValArgLeuAlaSerHisLeuArgLysLeuArgLysArgLeuLeuArgAspAlaAsp 153

Db 593 CGGGTGGCGCTCGCGCTCCACCTCGCAAGCTGCGTAAGCGGCTCTCCCGCATGCCGAT 534

Qy 154 AspLeuGlnLysArgLeuAlaValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGly 173

Db 533 GACCTGCAGAAAGCGCTTGCAGTGTACAGGCCGCGGCGCCGAGGGCGCCGAGCGCGC 474

Qy 174 LeuSerAlaIleArgGluArgLeuGlyProLeuValGluGlnGlyArgValArgAlaAla 193

Db 473 CTCAGCGCCATCCGCGAGCGCTGGGCGCCCTGGTGGAAACAGGGCGCGGTGCGGCGCC 414

Qy 194 ThrValGlySerLeuAlaGlyGlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArg 213

Db 413 ACTGTGGGCTCTCTGGCGCGCCAGCCCTACAGAGCGGGCGCCAGGCTGGGGCGAGCGG 354

Qy 214 LeuArgAlaArgMetGluGluMetGlySerArgThrArgAspArgLeuAspGluValLys 233

Db 353 CTGCGCGCGGATGGAGGATGGGAGCGCGGACCGCGCGCCGCGCGCTGGAGGTGAAG 294

Qy 234 GlnGlnValAlaGluValArgAlaLysLeuGluGlnAlaGlnGlnIleArgLeuGln 253

Db 293 GAGCAGGTGGCGGAGGTGCGCGCCAGCTGGAGGAGCGAGGCCAGCAGATACGCGCTGAG 234

Qy 254 AlaGluAlaPheGlnAlaArgLeuLysSerTrpPheGluProLeuValGluAspMetGln 273

Db 233 GCCAGGCGCTTCCAGGCGCGCTCAAGAGCTGGTTCGAGGCCCTTGGTGGAGAGATGCG 174

Qy 274 ArgGlnTrpAlaGlyLeuValGluLysValGlnAlaAlaValGlyThrSerAlaAlaPro 293

Db 173 CGCCAGTGGCGCGCGCTGGTGGAGAGGTGCGGTGCGGTGGGACCGACCGCGCCCT 114

Qy 294 ValProSerAspAsnHis 299

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RESULT 11

BM042094

LOCUS

DEFINITION

603615713F1 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:5420618 5',

mRNA sequence.

ACCESSION

BM042094

VERSION

BM042094.1 GI:16771361

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 800)

NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaaps-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLCM1875 row: i column: 03
 High quality sequence stop: 792.
 Location/Qualifiers

FEATURES

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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5420618"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 112"
 /notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 3,69e-96 Length: 800
 Score: 1111.00 Matches: 226
 Percent Similarity: 99.1% Conservative: 4
 Best Local Similarity: 97.4% Mismatches: 2
 Query Match: 74.4% Indels: 1
 DB: 2 Gaps: 0

US-09-827-854A-2 (1-299) x BM042094 (1-800)

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 DB 104 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGAGCCCGAGTGGCCAGCAGCGAGTGG 163
 QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGluArgPheTrpAspTyrLeuArgTrpVal 40
 DB 164 CAGAGCGCCAGCGCTGGGAACTGGCACTGGGTGGCTTTGGATACCTGGCTGGGTG 223
 QY 41 GlnThrLeuSerGluGlnValGlnGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
 DB 224 CAGACACTGTCTAGCAGAGTGCAGGAGGAGTGTCTAGCTCCAGGTCACCCAGGAATG 283
 QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
 DB 284 AGGCGCGTGTAGCAGGACCATGAAGAGTTGAAGGCCCTACAAATCGGAACCTGGAGAA 343
 QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
 DB 344 CAATGACCCCGTGGCGGAGGAGACCGCGGACCGCTGTCCAAGGAGCTGCAGGCGCG 403
 QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
 DB 404 CAGGCCCGCTGGCGCGGACATGGAGGAGCGTGTGCGCGCGCTGTGTGCAGTACCGCGC 463
 QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
 DB 464 GAGGTGCAGGCCCATGTCTCGGCCAGAGCACCAGAGAGCTGGCGGTGCGCCCTCCAC 523
 QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
 DB 524 CTGGCAAGTGGTAAAGCGGCTCTCTCGCGATGCCGATGACCTGCAGAGAGCGCTGCA 583
 QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaLeuArgGluArg 180
 DB 584 GTGTACCAAGCCCGGCGCGAGGCGCGAGCGCGCTTCAGCGCATCCCGAGCGC 643
 QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200

DB 644 CTGGGGCCCTGGTGAACAGGGCCCGCTGGGGCCAGCACTGTGGGCTCCCTGGCGGC 703
 QY 201 GlnProLeuGlnGlnArgAlaGlnAlaTrpGlyGluArgLeuAlaArgMetGluGlu 220
 DB 704 CAGCGCTACAGAGCGGCCAGGCTGGGGCGAGCGGTG-CGCGCGGATGGAGAG 762
 QY 221 MetGlySerArgThrArgAspArgLeuAspGluVal 232
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RESULT 12

BG472299
 LOCUS 602513830F1 NTH_MGC_16 Homo sapiens cDNA clone IMAGE:4645759 5',
 DEFINITION mRNA sequence.

ACCESSION BG472299.1 GI:13404485
 VERSION BG472299
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

1 (bases 1 to 927)

REFERENCE
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM1419 row: k column: 08
 High quality sequence stop: 848.
 Location/Qualifiers

FEATURES

source

1..927
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 /clone="IMAGE:4645759"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 16"
 /notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 4,97e-96 Length: 927
 Score: 1110.50 Matches: 257
 Percent Similarity: 91.8% Conservative: 2
 Best Local Similarity: 91.1% Mismatches: 13
 Query Match: 74.4% Indels: 12
 DB: 2 Gaps: 1

US-09-827-854A-2 (1-299) x BG472299 (1-927)

QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnThrGluTrp 20
 DB 101 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGAGCCCGAGTGGCCAGCAGTGG 160
 QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGluArgPheTrpAspTyrLeuArgTrpVal 40
 DB 161 CAGAGCGCCAGCGCTGGGAACCTGGCACTGGGTGGCTTTTGGGATTAACCTGGCGTGGGTG 220

Qy 41 GlnThrLeuSerGluGlnValGlnGluGluLeuSerSerGlnValThrGlnGluLeu 60
Db 221 CAGACACTGTCTGAGACAGTGCAGAGGAGTGTCTCAGCTCCAGGTCAACAGGAACTG 280
Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu 80
Db 281 AGGCGCTGATGGACGACCATGAAGGAGTTGAAGGCTTCAAAATCGAACTGGAGAA 340
Qy 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAla 100
Db 341 CAACCTGACCCCGGTGGCGAGAGACGCGGCACGCGTGTCCAAGGAGCTCGAGCGCG 400
Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 401 CAGCGCCGCTGGCGCGGACATGGAGGAGCTGTGCGGCCCTGTGTCAGTACCGCGCG 460
Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 461 GAGGTGCAGGCGCATGCTCGGCACAGACACCGAGGAGCTGCGGGTGCCTCGCTCCAC 520
Qy 141 LeuArgLysLeuArgLysArgLeuLeuLeuArgAlaAspAlaAspLeuGlnLysArgLeuAla 160
Db 521 CTGCGCAAGCTGCGTAAGCGGCTCTCTCGCGATGCCGATGACCTGCAGAGCGCTGCGCA 580
Qy 161 ValTyrGln-AlaGlyAlaArgGluGlyValaGluArgGly--LeuSerAlaIleArgGlu 179
Db 581 GTGTACACAGGCGCGGCGCGAGGCGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGG 640
Qy 180 ArgLeu--GlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuA 199
Db 641 CGCCTTGGGCGCCCTGGGTGGAACAGAGGCGCGGCTGCGGGCGCGCACGTGTGGGCTCCCTGG 700
Qy 199 laGlyGlnProLeuGlnGluArgAlaGlnAlaThrGlyArgLeuArgAlaArgMetG 219
Db 701 CCGGCCACGCG-CTACAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 758
Qy 219 luGluMetGlySerArg-ThrArgAspArgLeuAspGluValLysGluGlnValAlaGlu 238
Db 759 AGGAGATGGGCGAGCGGACCGCGACCGCGACCGCTGGACCGAGGTGAAGGACGAGTGGCGGAG 818
Qy 239 -ValArgAlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAla---Ph 257
Db 819 GGTGCGCGCGAAGCTGGAGGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 878
Qy 257 eGlnAlaArg-LeuLysSerTrpPhe-GluProLeuValGluAspMet 272
Db 879 CAGGCGCGCGGCGCTCAAGAGCTGTGTTGCGAGCGGCTGGGTGGAAGACATG 926

RESULT 13

LOCUS B1597743 922 bp mRNA linear EST 07-SEP-2001
DEFINITION 603248609F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5300259 5',
mRNA sequence.

ACCESSION B1597743

VERSION B1597743.1 GI:15490682

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

1 (bases 1 to 922)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11760 row: b column: 04
High quality sequence stop: 782.
Location/Qualifiers

FEATURES

source

1..922
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5300259"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(gcgag); Oligo-dr primed using primer
5'-TTTTTTTTTTTTTN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Alignment Scores: 9.57e-96 Length: 922
Pred. No.: 1107.50 Matches: 239
Score: 93.1% Conservative: 4
Percent Similarity: 91.6% Mismatches: 14
Best Local Similarity: 74.2% Indels: 5
Query Match: 2 Gaps: 1
DB:

US-09-827-854A-2 (1-299) x B1597743 (1-922)

Qy 1 LysValGluGlnAlaValGluThrGluProGluLeuArgGlnGlnThrGluTrp 20
Db 127 AAGGTGGAGCNAAGCGGTGGAGACAGAGCGCGGAGCTGCGCCAGCAGACCGAGTGG 186
Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 187 CAGAGCGCCAGCGCTGGAACTGGCACCTGGTGGCTTTTGGGATTACCTCGCTGGGTG 246
Qy 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 247 CAGACACTGTGTAGCAGAGGTGCAGAGGAGCTGTCTAGCTCCAGGTCCACCGAGAACTG 306
Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 307 AGGCGCTGTATGGACGAGACCATGAGAGATTGAAGGCTTACAATCGGAATCGAGGAA 366
Qy 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db 367 CAACCTGACCCCGGTGGCGAGGACAGCGGCGACGCGCTGTCCAAGGAGCTCGAGCGCG 426
Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 427 CAGCGCGGCTGGCGCGGACATGAGGACGCTGTGCGGCCCTGGTGCAGTACCGCGCG 486
Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 487 GAGGTGAGGCCATGCTCGGCCAGGACCGAGGAGCTGCGGGTGGCGCTCGCTCCCTCC 546
Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAlaAspAlaAspLeuGlnLysArgLeuAla 160
Db 547 CTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAGCGCTGCGCA 606
Qy 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
Db 607 GTGTACAGGCGCGGCGCGGAGGCGCGGAGCGGCTC-AGCGGCATCCCGGAGCGCG 665
Qy 181 LeuGlyProLeuVal-GluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaG1 200

Db 666 CTGGGGCCCTGGTGGAAACAGCGCGGGTGC CGCGCCGACCTGTGGGTCTCCCTGGCCGG 725
 Qy 200 yGln-ProLeuGlnArg-AlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGlu 219
 Db 726 CCAGCCCGCTACAGGAGCGGGCCCGAGGCTGGGGCGAGCGGATACGCGCGGATGAGCG 785
 Qy 220 GluMetGlySerArgThrArgAepArgLeuAspGluValysGluGlnValAlaGluVal 239
 Db 786 AGCAGGGGCGCGGACCGAGACCGCTGGACGAGGTGAAGAGAGAGGTGGCGGGGGTG 845
 Qy 240 ArgAlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGln 258
 Db 846 GGGCCCAAGCTGAAGAAACAGCCAGAAATACGCTTA---GCCGAAGGCTTCAGG 899

RESULT 14

BM728696 706 bp mRNA linear EST 01-MAR-2002
 LOCUS UI-E-EJO-aiu-1-08-0-UI.r1 UI-E-EJO Homo sapiens cDNA clone
 DEFINITION UI-E-EJO-aiu-1-08-0-UI 5', mRNA sequence.

ACCESSION BM728696.1 GI:19050022

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

1 (bases 1 to 706)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL

PUBMED

COMMENT

Contact: Soares, MB
 8889548
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: Mlj Reverse.

FEATURES

#source

1..706
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-EJO-aiu-1-08-0-UI"
 /tissue_types="fetal eyes, lens, eye anterior segment,
 optic nerve, retina, Retina Foveal and Macular, RPE and
 Choroid"
 /dev_stage="fetal and adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-EJO"
 /notes="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
 modified polylinker; Site 1: Ecor I; Site 2: Not I;
 UI-E-EJO is a subtracted cDNA library constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an Ecor I adaptor, digested
 with Not I, and cloned directionally into pT7T3-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tags for this library are: fetal eyes,
 AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment,

AATGCCGAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina
 Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This
 library was created for the program, Gene Discovery in the
 Visual System, supported by National Eye Institute (NEI).

ORIGIN

Alignment Scores:

Pred. No.: 1,48e-95 Length: 706
 Score: 1104.00 Matches: 228
 Percent Similarity: 98.3% Conservative: 0
 Best Local Similarity: 98.3% Mismatches: 2
 Query Match: 73.9% Indels: 2
 DB: 3 Gaps: 0

US-09-827-854A-2 (1-299) x BM728696 (1-706)

Qy 1 LysValGluGlnAlaVal-GluThrProGluProGluLeuArgGlnGlnThrGluTr 20
 Db 14 AAGGTGGAGCAACGGTGGAGACAGACGCGGAGCCGAGCTGCGCAGACCGAGTG 73
 Qy 20 pGlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArg-TrpV 40
 Db 74 GCAGAGCGCGCCAGCGCTGGGAACCTGGCACTGGGTGCTTTGGGATTACCTGCGCGTGG 133
 Qy 40 alGlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluL 60
 Db 134 TGCAGACACTGTCTGAGCAGGTGTCAGAGAGGTGCTCAGTCCAGTCCAGGTCCACCGAAG 193
 Qy 60 euArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluG 80
 Db 194 TGAGGGCGGTGTGGACGAGACCATGAAGAGTTGAAGGCTTACACATCGGAATGTGAGG 253
 Qy 80 luGlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaA 100
 Db 254 AACAACTGACCCCGTGGCGGAGGAGACCGCGGACGGCTGTCCAAGGAGCTGCAGGCGG 313
 Qy 100 laGlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgG 120
 Db 314 CGCAGCGCGCGCTGGCGCGCGACATGAGAGACATGCGCGCGCGCTTGGTGCAGTACCGCG 373
 Qy 120 lyGluValGlnAlaMetLeuGlyGlnSerThrGluLeuArgValArgLeuAlaSerH 140
 Db 374 GCAGGTGGAGGCGCATGTCTGGCCAGACAGCAGGAGCTGCGGGTGGCGCTCGCTCC 433
 Qy 140 isLeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuA 160
 Db 434 ACCTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAGCGCGCTGG 493
 Qy 160 laValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluA 180
 Db 494 CAGTGTACCAGCGCGGCGCGCGAGCGCGCGCGCGCTCTCAGCGCATCCGCGAGC 553
 Qy 180 rGluGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaG 200
 Db 554 GCCTGGGGCCCCCTGGTGGAAACAGCGCGCGCTGCGGGCGCCCATGTGGGCTCTCTGCGCG 613
 Qy 200 lyGlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluG 220
 Db 614 GCCAGCGCTACAGGAGCGGCGCCAGGCTGGGGCGAGCGGCTGCGCGCGCGGATGAGG 673
 Qy 220 luMetGlySerArgThrArgAspArgLeuAsp 230
 Db 674 AGATGGCGCGCGGACCCCGACCGCTGGAC 705

RESULT 15

BF967543/c

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

BF967543 954 bp mRNA linear EST 23-JAN-2001
 602287404T1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4374576 3',
 mRNA sequence.
 BF967543
 BF967543.1 GI:12334758
 EST.
 Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

1 (bases 1 to 954)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence start: 16

High quality sequence stop: 839.

FEATURES

source

1..954

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4374576"

/tissue_type="hypothalamus"

/lab_host="DH10B"

/clone_lib="NIH_MGC_96"

/notes="Organ: brain; Vector: pBluescriptR (modified

pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI

(gtcgag); Oligo-dT primed using primer

5'-TTTTTTTTTTTTTNN-3', size-selected for average

insert size 2.3 kb and normalized to ROT 5. This is a

primary library enriched for full-length clones and

constructed using the Cap-trapper method (Carninci, in

preparation). Library constructed by M. Brownstein

(NIH/NHGRI, National Institutes of Health). Note: this is

a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	6,53e-95	Length:	954
Score:	1099.00	Matches:	243
Percent Similarity:	95.4%	Conservative:	4
Best Local Similarity:	93.8%	Mismatches:	6
Query Match:	73.6%	Indels:	7
DB:	2	Gaps:	0

US-09-827-854a-2 (1-299) x BP67543 (1-954)

QY	47	ValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu-ArgAla-LeuMetAspG	66
Db	883	GTCCAGGAGGAGCTGTTTCAGCTCCAGAGTCAACCAGGAACCTGGAGGGCGCTTGATGGACG	824
QY	66	IuThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu-GlnLeuThrProVal	85
Db	823	AGACCATGAGGAGTGAAGCCTACAAATCGGAACCTGGAGGAACCACTGACCCCGGTG	764
QY	86	AlaGluGluThr-ArgAlaArgLeuSer--LysGluLeuGlnAlaAlaGlnAlaArgLeu	104
Db	763	GCGGAGGAGACGGCGGCACGGCTGTCCAGGAGGAGCTGCAGGGCGGCAGGCCCGGCTG	704
QY	105	GlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGlyGluValGlnAla	124
Db	703	GGCGCGACATGGAGGACGTGTGGCGCGCCCTGTCAGTACCAGCGCGAGGTGCAGGCC	644
QY	125	MetLeuGlyGlnSerThrGluLeuArgValArgLeuAlaSerHisLeuArgLysLeu	144
Db	643	ATGCTCGCGCAGAGCACCGAGGAGCTGGGGTGGCGCTTCGCCTCCACCTGCGCAAGCTG	584
QY	145	ArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAlaValTyrGlnAla	164

Search completed: June 15, 2006, 00:06:14

Job time : 7925.48 secs

Db	583	CGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGTGTACAGGCC	524
QY	165	GlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArgLeuGlyProLeu	184
Db	523	GGGGCCCGCAGGGCGCGCGCTCAGCGCCATCCGCGAGCGCTGGGGCCCTG	464
QY	185	ValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGlyGlnProLeuGln	204
Db	463	GTGGACGGGGCGCGTGGCGCGCCACCTGTGGGCTC-CTGGCGCGCCAGCCGCTACAG	405
QY	205	GluArgAlaGlnAlaThrGlyGluArgLeuArgAlaArgMetGluGluMetGlySerArg	224
Db	404	GAGCGGGCCAGGCGCTGGGGCGAGCGGCTGCGCGCGGATGGAGGAGATGGGCGAGCGG	345
QY	225	ThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArgAlaLysLeuGlu	244
Db	344	ACCGCGACCGCTGGACGAGGTGAAGGACAGGTGGCGGAGGTGCGCGCAAGCTGGAG	285
QY	245	GluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArgLeuLysSerTrp	264
Db	284	GAGCAGGCCAGCAGATACGCTGCAGCGCGAGGCTTCAGGCGCGCTCAAGAGCTGG	225
QY	265	PheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuValGluLysValGln	284
Db	224	TTCGAGCCCTGTTGGAAGACATGCAGCGCCAGTGGGCGCGGCTGTGGAGAGGTGCAG	165
QY	285	AlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis	299
Db	164	GCTGCCGTGGGCACCGCGCGCCCTGTGCCAGCGCAACAATCAC	120

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 19:03:31 ; Search time 312.205 seconds
(without alignments)
2687.952 Million cell updates/sec

Title: US-09-827-854A-2

Perfect score: 1493

Sequence: 1 KVEQAVETEPELQQTEW.....VEKQAAVGTSAAPVPSDNH 299

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Database :

Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1493	100.0	1156	3	US-09-023-655-1007 Sequence 1007, Ap
2	1493	100.0	1291	3	US-09-919-039-246 Sequence 246, App
3	1484	99.4	1157	2	US-07-709-949-1 Sequence 1, Appli
4	1484	99.4	1157	4	US-09-880-107-2244 Sequence 2244, Ap
5	1363.5	91.3	3805	3	US-09-108-006C-3 Sequence 3, Appli
6	1082	72.5	1126	3	US-08-949-155-5 Sequence 5, Appli
7	1082	72.5	1126	3	US-09-819-964-5 Sequence 5, Appli
8	1026	68.7	664	4	US-10-211-689-37 Sequence 37, Appl

9	1026	68.7	718	4	US-10-211-689-35 Sequence 35, Appl
10	1026	68.7	802	4	US-10-211-689-31 Sequence 31, Appl
11	997	66.8	652	4	US-10-211-689-43 Sequence 43, Appl
12	997	66.8	709	4	US-10-211-689-41 Sequence 41, Appl
13	997	66.8	788	4	US-10-211-689-33 Sequence 33, Appl
14	992	66.4	4267	3	US-08-949-155-51 Sequence 51, Appl
15	992	66.4	4267	3	US-09-819-964-51 Sequence 51, Appl
16	973	65.2	691	4	US-10-211-689-45 Sequence 45, Appl
17	892	59.7	660	2	US-08-726-306A-28 Sequence 28, Appl
18	855	57.3	616	4	US-10-211-689-39 Sequence 39, Appl
19	805.5	54.0	684	4	US-10-211-689-29 Sequence 29, Appl
c 20	533	35.7	478	4	US-09-880-107-2491 Sequence 2491, Ap
21	511	34.2	330	2	US-07-849-389-6 Sequence 6, Appli
22	412	27.6	405	3	US-09-513-999C-2137 Sequence 2137, Ap
23	374	25.1	252	3	US-08-617-256-24 Sequence 24, Appl
24	374	25.1	252	3	US-09-287-141-24 Sequence 24, Appl
25	374	25.1	252	3	US-09-431-613-24 Sequence 24, Appl
26	374	25.1	252	3	US-09-504-245-24 Sequence 24, Appl
27	374	25.1	252	3	US-09-287-682-24 Sequence 24, Appl
28	374	25.1	252	3	US-09-287-679-24 Sequence 24, Appl
29	374	25.1	252	3	US-09-397-766-24 Sequence 24, Appl
30	374	25.1	252	3	US-09-287-681-24 Sequence 24, Appl
31	374	25.1	252	3	US-09-495-444-24 Sequence 24, Appl
32	374	25.1	252	3	US-09-796-416-24 Sequence 24, Appl
33	374	25.1	252	3	US-09-879-341-24 Sequence 24, Appl
34	374	25.1	252	3	US-09-724-877-24 Sequence 24, Appl
35	374	25.1	372	3	US-09-621-976-1386 Sequence 1386, Ap
36	332	22.2	258	3	US-09-490-609B-149 Sequence 149, App
37	258.5	17.3	1469	3	US-09-949-016-4983 Sequence 4983, Ap
38	224	15.0	121	3	US-09-818-875-3400 Sequence 3400, Ap
c 39	224	15.0	121	3	US-09-818-875-3401 Sequence 3401, Ap
40	219	14.7	121	3	US-09-818-875-3404 Sequence 3404, Ap
c 41	219	14.7	121	3	US-09-818-875-3405 Sequence 3405, Ap
42	210	14.1	7065	3	US-09-874-923-115 Sequence 115, App
43	205.5	13.8	6604	3	US-09-949-016-16725 Sequence 16725, A
44	198	13.3	121	3	US-09-818-875-3464 Sequence 3464, Ap
c 45	198	13.3	121	3	US-09-818-875-3465 Sequence 3465, Ap

ALIGNMENTS

RESULT 1

US-09-023-655-1007

; Sequence 1007, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023.655

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

```
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1007:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1156 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g178850
; US-09-023-655-1007

Alignment Scores:
Pred. No.: 3,86e-135 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-2 (1-299) x US-09-023-655-1007 (1-1156)
QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnThrGluTrp 20
Db 115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGAGCCGAGCTGCGCCAGCAGACCGAGTGG 174
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 175 CAGAGCGGCAGCGCTGGGAACTGGCACTGGTTCGCTTTGGATTACCTGCGCTGGGTG 234
QY 41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGTCTAGCTCCAGAGTCAACCCAGGAATG 294
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu 80
Db 295 AGGCGCTGTATGACGAGACCATGAAGAGTTGAAGCGCTACAAATCGGAACCTGGAGAA 354
QY 81 GlnLeuThrProValAlaGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db 355 CAACCTGACCCCGTGGCGGAGGAGACGCGGCGACGCTGTCCAAGGAGCTGCAGGCGCG 414
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 415 CAGGCGCGCTGGCGCGGACATGGAGGACGTGTGCGCGCGCTGTGTCAGTACCGCGGC 474
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 475 GAGGTGAGGCCATGCTCGGCCAGAGCACCAGAGAGCTGCGGGTGCCTTCGCCCTCCAC 534
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
Db 535 CTGCGCAAGCTGCGTAAAGCGCTCTCCGCGATCCGATGACCTGCAGAGCGCTGCCA 594
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaLeuArgGluArg 180
Db 595 GTGTACCAAGCCGGGCGCGAGGCGCGGAGCGCGCTTCAGCGCATCCCGAGCGC 654
QY 181 LeuGlyProLeuValGlnGlnArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 655 CTGGGGCGCTGTGGTGAACAGGCGCGCTGGGGCGCGCCACTGTGGGCTTCCTGGCGCG 714
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
Db 715 CAGCGCTACAGAGCGGCGCCAGGCTTGGGCGAGCGGCTGTGCGCGCGGATGGAGAG 774
QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
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Db 775 ATGGGCAGCCGACCCGACCCGCTTGGACGAGGTGAAGAGCAGGTGGCGGAGGTGGCG 834
QY 241 AlaLysLeuGluGlnAlaGlnGlnAlaArgLeuGlnAlaPheGlnAlaArg 260
Db 835 GCCAAGCTGAGGAGCAGCCAGCAGATACGCTGCAGGCGGAGGCTTCAGGCGCGC 894
QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db 895 CTCAGAGAGCTGGTTCAGGCGCTTGGTGAAGACATGACGCGCAGTGGCGCGGCTGGTG 954
QY 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAlaHis 299
Db 955 GAGAGGTGAGGCTGCGGTGGGACACAGCGCGCCCTGTGCCCCAGCAATCAC 1011

RESULT 2
US-09-919-039-246
; Sequence 246, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 246
; LENGTH: 1291
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 2514988CB1
; NAME/KEY: unseq
; LOCATION: 46
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-246

Alignment Scores:
Pred. No.: 4,47e-135 Length: 1291
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-2 (1-299) x US-09-919-039-246 (1-1291)
QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnThrGluTrp 20
Db 240 AAGGTGAGCAAGCGGTGGAGACAGAGCCGAGCCGAGCTGCGCCAGCAGACCGAGTGG 299
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 300 CAGAGCGCGCAGCGCTGGGAACTGGCACTGGTTCGCTTTGGATTACCTGCGCTGGGTG 359
QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 360 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGTCTAGCTCCCAAGGTCAACCCAGAACTG 419
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 420 AGGCGCTGTATGACGAGACCATGAAGAGTTGAAGCGCTACAAATCGGAACCTGGAGAA 479
QY 81 GlnLeuThrProValAlaGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db 480 CAACCTGACCCCGTGGCGGAGGAGACGCGGCGACGCTGTCCAAGGAGCTGCAGGCGCG 539
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
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Db 540 CAGGCCGGCTGGCGCGCGACATGGAGGACGTGTGCGCGCGCTGGTGCAGTACCGCGC 599
Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrCluLueuArgValArgLeuAlaSerHis 140
Db 600 GAGGTGAGGCGCATGCTGGCGCAGACCGAGAGAGTGGCGGTGCCTGCGCTCCAC 659
Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
Db 660 CTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAGCGCTGGCA 719
Qy 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGlnArgGlyLeuSerAlaIleArgGluArg 180
Db 720 GTGTACAGGCGGGCGCGAGGCGCGAGCGCGCTCAGCGCGCTCAGCGCATCCGCGAGCGC 779
Qy 181 LeuGlyProLeuValGluGlnGlyValArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 780 CTGGGGCCCTGTGTGGAACAGGGCGGTGGGGCGCCCACTGTGGGCTCCCTGGCGCGC 839
Qy 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
Db 840 CAGCGCTACAGAGCGGGCGCCAGCGCTGGGGCGAGCGGTGCGCGCGGATGGAGAG 899
Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 900 ATGGGCAAGCGGACCGCGCGCGCTGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 959
Qy 241 AlaLysLeuGluGlnGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 960 GCCAAGCTGGAGGAGCAGGCGCCACAGATACGCTGCAGGCGGAGGCTTCCAGGCGCGC 1019
Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db 1020 CTCAGAGCTGTTTCGAGCGCCCTGTGTGAAGACATGCGCGCCAGTGGCGCGGCTGGT 1079
Qy 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 1080 GAGAAAGTGCAGGCTGCGTGGGCGACCGCGCGCGCGCTGTGCCCGAGCGACAATCAC 1136

RESULT 3

US-07-709-949-1

; Sequence 1, Application US/07709949

; Patent No. 5472858

; GENERAL INFORMATION:

; APPLICANT: Attie, Alan D

; APPLICANT: Gretch, Daniel G

; APPLICANT: Sturley, Stephen L

; APPLICANT: Beckage, Nancy E

; TITLE OF INVENTION: Production of Recombinant Proteins in

; TITLE OF INVENTION: Insect Larvae

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Quarles & Brady

; STREET: P.O. Box 2113

; CITY: Madison

; STATE: WI

; COUNTRY: USA

; ZIP: 53701-2113

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/07709,949

; FILING DATE: 19910604

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Seay, Nicholas J

; REGISTRATION NUMBER: 27,386

; REFERENCE/DOCKET NUMBER: 9629691801

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 251-5000

; TELEFAX: (608) 251-9166

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1157 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 62..1015

; FEATURE:

; NAME/KEY: misc signal

; LOCATION: 62..119

; PUBLICATION INFORMATION:

; AUTHORS: McLean, J W

; JOURNAL: Journal of Biological Chemistry

; VOLUME: 259

; PAGES: 6498-6504

; DATE: 1984

; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1157

US-07-709-949-1

Alignment Scores:

Pred. No.: 2,86e-134 Length: 1157

Score: 1484.00 Matches: 297

Percent Similarity: 99.3% Conservative: 0

Best Local Similarity: 99.3% Mismatches: 2

Query Match: 99.4% Indels: 0

DB: 2 Gaps: 0

US-09-827-854A-2 (1-299) x US-07-709-949-1 (1-1157)

Qy 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
Db 116 ARGGTGAGCAGCGGTGGAGACAGAGCCGAGCCGAGCTGCCAGCAGCAGCTGG 175
Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 176 CAGAGCGCCAGCGCTGGGAACCTGGCACTGGTGCCTTTTGGGATTACCTGGCGTGGGTG 235
Qy 41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 236 CAGACACTGTCTGAGCAGGTGCAGGAGAGCTGTCTCAGCTCCCAAGTCACCCAGAACTG 295
Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 296 AGGCGCTGATGACGAGACCATGAGGAGTTGAGGCGCTTACAATCGGAACCTGGAGAA 355
Qy 81 GlnLeuThrProValAlaGluThrArgAlaArgLeuSerTyrGluLeuGlnAlaAla 100
Db 356 CAACTGACCCCGGTAGCGGAGGAGACGCGGCGCTGTCCAAGGAGCTGCAGACGCGC 415
Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 416 CAGCGCCGCTGGCGCGGACATGGAGAGACGTGTGTGCGCGCGCTGTGTGTACCGCGC 475
Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 476 GAGTGCAGGCCATGCTCGGCCAGAGCAGCAGAGAGTGGGGTGGCGCTCCCTCCAC 535
Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
Db 536 CTGGCAAGCTGCGTAAGCGGCTCTCCGCGATCCCGATGACCTGCAGAGCGCTGGCA 595
Qy 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
Db 596 GTGTACCGCGCGCGCGCGAGCGCGCGAGCGCGCTCAGCGCATCCCGCGAGCGC 655

QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
DB 656 CTGGGGCCCTGGTGGAAACAGGGCCGGTGGGGCCGCCACTGTGGGCTCCCTGGCCGGC 715
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
DB 716 CAGCCGCTACAGAGCGGGCCAGGCTGGGGCGAGCGGTGCGCGCGGATGGAGGAG 775
QY 221 MetGlySerArgThrArgArgLeuAspGluValGluGlnValAlaGluValArg 240
DB 776 ATGGGAGCTGGACCCCGACCCCTGGACAGAGGTGAAGAGAGAGGTGGGGAGGTGGC 835
QY 241 AlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
DB 836 GCCAAGCTGGAGGAGCAGGCCCGACAGATACGCTGCAGGCCGAGGCTTCAGGCCCGC 895
QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
DB 896 CTCAAGAGCTGGTTCGAGGCCCTGGTGGAGACATGCAGGCCAGTGGGCGGGCTGGTG 955
QY 281 GluLysValGlnAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
DB 956 GAGAAGGTGAGGCTGCGTGGGACACAGCGCCGCTGTGCCCGAGCAATCAC 1012

RESULT 4

US-09-880-107-2244
; Sequence 2244, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2244
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 M12529
US-09-880-107-2244

Alignment Scores:
Pred. No.: 2,86e-134 Length: 1157
Score: 1484.00 Matches: 297
Percent Similarity: 99.3% Conservative: 0
Best Local Similarity: 99.3% Mismatches: 2
Query Match: 99.4% Indels: 0
DB: 4 Gaps: 0

US-09-827-854A-2 (1-299) x US-09-880-107-2244 (1-1157)

QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnThrGluTrp 20
DB 116 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCGAGCTGCGCCAGCAGACGAGTGG 175
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTrpLeuArgTrpVal 40
DB 176 CAGAGCGCGCAGCGCTGGGAACCTGGCTGGTGGCTTTGGGATTACCTGCGCTGGGTG 235
QY 41 GlnThrLeuSerGluGlnValGlnGluGluLeuSerSerGlnValThrGlnGluLeu 60
DB 236 CAGACACTGTCTGAGCAGGTGACAGGAGAGTGTCTAGTCCCAAGTCAACCAAGAACTG 295

QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrlYsSerGluLeuGluGlu 80
DB 296 AGGGCGCTGATGGACAGAGACCATGAAGAGATTGAAGGCCCTACAAATCGGAATCGGAGGA 355
QY 81 GlnLeuThrProValAlaGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
DB 356 CAACTGACCCCGGTAGCGAGGAGAGCGCGGACGCGCTGTCCAAGGAGCTGCAGACGCGC 415
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTrpArgGly 120
DB 416 CAGGCCCGCTGGGCGCGGACATGGAGGACGTGTGGCGCGCTGGTGCAGTACCGCGGC 475
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
DB 476 GAGGTGACGCCATGCTCGGCCAGAGCACCGAGGAGCTGGGTGGCGCTCGCTCCAC 535
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
DB 536 CTGCGCAAGCTCGTAAAGCGCTCTCCCGCATCCCGATGACCTGCAGAGCCCTGGCA 595
QY 161 ValTyrlGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
DB 596 GTGTACACAGCGCGGCGCGCGAGGCGCGAGCGCGCTCAGCGCCATCCCGAGCGC 655
QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
DB 656 CTGGGGCCCTGGTGGAAACAGGCCCGCTGGGGCCGCCACTGTGGGCTCCCTGGCGGC 715
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
DB 716 CAGCCGCTACAGAGCGGGCCCGCGCGAGCGCGCTGGCGCGCGGATGGAGGAG 775
QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
DB 776 ATGGGAGCTGGACCCCGACCCCTGGACAGGTGAGGAGCAGGTGGCGGAGGTGGC 835
QY 241 AlaLysLeuGluGlnGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
DB 836 GCCAAGCTGGAGGAGCAGGCCCGACAGATACGCTGCAGGCCGAGGCTTCAGGCCCGC 895
QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
DB 896 CTCAAGAGCTGGTTCGAGGCCCTGGTGGAGACATGCAGGCCAGTGGGCGGGCTGGTG 955
QY 281 GluLysValGlnAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
DB 956 GAGAAGGTGAGGCTGCGTGGGACACAGGCCCGCTGTGCCCGAGCAATCAC 1012

RESULT 5

US-09-108-006C-3
; Sequence 3, Application US/09108006C
; Patent No. 6524613
; GENERAL INFORMATION:
; APPLICANT: Steer, Clifford J.
; Kren, Betsy T.
; Bandyopadhyay, Paramita
; Roy-Chowdhury, Jayanta
; TITLE OF INVENTION: Hepatocellular Chimeraplasty
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kimeragen, Inc.
; STREET: 300 Pheasant Run
; CITY: Newtown
; STATE: PA
; COUNTRY: USA
; ZIP: 18940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,006C

;; FILING DATE: 30-Jun-1992
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/054,288
;; FILING DATE: 30-APR-1997
;; APPLICATION NUMBER: 60/054,837
;; FILING DATE: 05-AUG-1997
;; APPLICATION NUMBER: 60/064,996
;; FILING DATE: 10-NOV-1997
;; APPLICATION NUMBER: 60/074,497
;; FILING DATE: 12-FEB-1998
;; APPLICATION NUMBER: PCT US 98/08834
;; FILING DATE: 30-APR-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Friebe, Thomas
;; REGISTRATION NUMBER: 29258
;; REFERENCE/DOCKET NUMBER: 7991-015-999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-504-4444
;; TELEFAX: 215-504-4545
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3805 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
;; FEATURE:
;; NAME/KEY: exon
;; LOCATION: 71...114
;; OTHER INFORMATION: Exon 1
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-108-006C-3

Alignment Scores:

Pred. No.:	6.27e-122	Length:	3805
Score:	1363.50	Matches:	298
Percent Similarity:	60.4%	Conservative:	0
Best Local Similarity:	60.4%	Mismatches:	1
Query Match:	91.3%	Indels:	195
DB:	3	Gaps:	1

US-09-827-854A-2 (1-299) x US-09-108-006C-3 (1-3805)

Qy	1	LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp	20
Db	2042	AAGGTGGAGCAAGCGGTGGAGACAGACCGAGCTGCGCCAGCAGACCGAGTGG	2101
Qy	21	GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal	40
Db	2102	CAGAGCGCCAGCGCTGGAACTGGCACTGGGTGCTTTTGGGATTACCTCGCTGGGTG	2161
Qy	41	GlnThrLeuSerGluGlnValGlnGluGlnGluLeuSerSerGlnValThrGlnGluLeu	60
Db	2162	CAGACACTGTCAGCAGAGTGCAGGAGGAGTGTCTAGCTCCAGGTCACCCAGGA	2220
Qy	60	-----	60
Db	2221	GAGGTGAGTGTCTCCCATCTGGCCCTTGACCCCTCTGTGGTGGCGGTATACCTCC	2280
Qy	60	-----	60
Db	2281	TCAGGTTTCATTTGCGCCCTGTGCGCTAAGTCTTTGGGGGGCGCTCGGTCTCTG	2340
Qy	60	-----	60
Db	2341	AGCTTCCTCTCCCATTTCTGACTCTCTGGCTTTAGTCTCTGGAATTTCTCTCTC	2400
Qy	60	-----	60
Db	2401	TTGTCTCTCTCTTCCCTTCTGACTCAGTCTCTCACACTCGTCTCTGGCTCTGTCT	2460

RESULT 6

Qy	60	-----	60
Db	2461	CTTCCCTAGCTCTTTTATATAGACAGAGATGGGGTCTCACTGTGTGGCCAGGCT	2520
Qy	60	-----	60
Db	2521	GGTCTTGAACCTTCTGGGCTCAAGGATCCTCCGCTCGGCTCCCAAAGTCTGGATT	2580
Qy	60	-----	60
Db	2581	AGAGCATGAGCACCTTGCCCGGCTCTAGCTCTCTTCTGTCTCTGCTCTGCTCTC	2640
Qy	60	-----	60
Db	2641	GCATCTGCTCTCTGCATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	2700
Qy	60	-----	60
Db	2701	TCCCTCTTGGTCTCTCTGGCTCATCCCATCTCGCGCCCATCCAGCCCTTCTCCC	2760
Qy	61	-----	66
Db	2761	CGCCTCCCACTCTGCGACACCTCCGCGCTCTCGGCGCGAGGGCGCTGATGACAG	2820
Qy	67	ThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlnLeuThrProValAla	86
Db	2821	ACCATGAAGAGTTGAAGGCTCAAAATCGAACTGGAGGAACAACCTGACCCCGGTGG	2880
Qy	87	GluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaGlnAlaArgLeuGlyAla	106
Db	2881	GAGGAGACGGCGGACGCTGTCTCAAGGAGTGCAGCGCGCGAGGCCCGCTGGCGCG	2940
Qy	107	AspMetGluAspValCysGlyArgLeuValGlnTyrArgGlyGluValGlnAlaMetLeu	126
Db	2941	GACATGGAGGACGTGTCTGGCGCGCTGTGTGAGTACCGCGCGAGGTGACGCCATGTCTC	3000
Qy	127	GlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHisLeuArgLysLeuArgLys	146
Db	3001	GGCCAGAGCACCAGGAGGCTGCGGGTGGCTCTCCCTCCCACTGCGGCAAGCTGGTAAG	3060
Qy	147	ArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAlaValTyrGlnAlaGlyAla	166
Db	3061	CGGCTCTCGCGATGCGGATGACCTGCAGAGGCGCTGGCAGTGTACCGAGCGCGGCGC	3120
Qy	167	ArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArgLeuGlyProLeuValGlu	186
Db	3121	CGCAGAGGCGCCGAGCGCGCTCAGCGCCATCCGCGAGCGCTGGGGCCCTTGTGGAA	3180
Qy	187	GlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGlyGlnProLeuGlnArg	206
Db	3181	CAGGGCCGCTGCGGGCGGCACTGTGGGCTCTCTGCGCGCCAGCGCTACAGAGCGG	3240
Qy	207	AlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGluMetGlySerArgThrArg	226
Db	3241	GCCCAGGCTTGGGCGAGCGGCTGCGCGCGGATGAGGAGATGGGCGAGCGGACCGCGC	3300
Qy	227	AspArgLeuAspGluValLysGluGlnValAlaGluValArgAlaLysLeuGluGln	246
Db	3301	GACCGCTTGAAGAGTGAAGGAGCAGGTGGCGAGGTGGCGCGCAAGCTGAGAGAGCAG	3360
Qy	247	AlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArgLeuLysSerTrpPheGlu	266
Db	3361	GCCCAGCAGATACCTCTGCGGCGAGGCTTCCAGGCGCGCTTCAAGAGCTGTTCCAG	3420
Qy	267	ProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuValGluLysValGlnAlaAla	286
Db	3421	CCCCTGTTGAAGACATGACGCGCAGTGGGCGGCTGTGTGGAGAGGTGACAGGCTGCC	3480
Qy	287	ValGlyThrSerAlaAlaProValProSerAspAsnHis	299
Db	3481	GTGGGCAACGAGCGCGCGCTGTGTGCCAGCGACAATCAC	3519

:	APPLICATION NUMBER:	08/949,155
:	FILING DATE:	<Unknown>
:	APPLICATION NUMBER:	US 60/046,094
:	FILING DATE:	09-MAY-1997
:	ATTORNEY/AGENT INFORMATION:	
:	NAME:	Hibler, David W.
:	REGISTRATION NUMBER:	41,071
:	REFERENCE/DOCKET NUMBER:	TAMK:177
:	TELECOMMUNICATION INFORMATION:	
:	TELEPHONE:	(512) 418-3000
:	TELEFAX:	(713) 789-2679
:	INFORMATION FOR SEQ ID NO:	5:
:	SEQUENCE CHARACTERISTICS:	
:	LENGTH:	1126 base pairs
:	TYPE:	nucleic acid
:	STRANDEDNESS:	single
:	TOPOLOGY:	linear
:	FEATURE:	
:	NAME/KEY:	CDS
:	LOCATION:	51..1001
:	SEQUENCE DESCRIPTION:	SEQ ID NO: 5:
:	US-09-819-964-5	

Qy	204	GlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaAargMetGluGluMetGlySer	223
Db	711	CGCGAGCGCGGAAGCCTGGGCCCAAGAAGTCGCAGACGGTCCGAGGAGATGGGCAGC	770
Qy	224	ArgThrArgAspArgLeuaspGluValLysGluGlnValalagAluValalagAlaLysLeu	243
Db	771	CGGACC CGCGACCGCCCTGGATGAGATGCGTGAGCAGCTGGAGGAGGTGGCGACCAAAGTG	830
Qy	244	GluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArgLeuLysSer	263
Db	831	GAGGAGCAGGCGCACCGCAGTTGCGCTTCAGCGCCGAGGGATTCCACGCCCTCTCCAAGGC	890
Qy	264	TrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuValGluLysVal	283
Db	891	TGGTTTCAGCCTCTCGTGGAAAGACATACGCGCCAGTCGGCGCCGGCTGGTGGAGAGCATG	950
Qy	284	GlnAlaAlaValGly---ThrSerAlaAlaProValProSerAspAsn	298
Db	951	CAGTCGCGCGGTGAGCATAGCTCTCTCCACTCTTCGCCGCCGAGTATAAT	998
RESULT 8			
US-10-211-689-37			

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; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 37
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(664)
US-10-211-689-37

Alignment Scores:
Pred. No.: 2,62e-90 Length: 664
Score: 1026.00 Matches: 214
Percent Similarity: 71.6% Conservative: 0
Best Local Similarity: 71.6% Mismatches: 1
Query Match: 68.7% Indels: 84
DB: 4 Gaps: 1

US-09-827-854A-2 (1-299) x US-10-211-689-37 (1-664)

QY 1 LysValGluGlnAlaValGluThrGluProGluLeuArgGlnGlnThrGluTrp 20
Db 11 AGGTGGAGCAAGCGTGGAGACAGAGCCGAGCGCCGAGCGCCAGACCGAGTGG 70
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 71 CAGAGCGGCGAGCGCTGGGAACCTGGCACTGGGTGCTTTTGGGATTAACCTGGCGTGGTG 130
QY 41 GlnThrLeuSerGluGlnValGlnGluGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 131 CAGACACTGCTGAGCAGGTGAGGAGAGAGCTGCTCAGCTCCAGGTCCACCCAGGAACTG 190
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 191 AGGGCGCTGATGACGAGACCATGAAGGATTGAAGGCTTACAAATCGGAACCTGGAGGAA 250
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db 251 CCACTGACCCCGTGGCGGAGGAGACGCGGCGCGCTGTCTCAAGGAG----- 298
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 298 ----- 298
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 298 ----- 298
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 298 ----- 298
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
Db 298 ----- 298
QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 299 CTGGGGCCCTGTTGGAAACAGGGCGCGGTGGGGCGCCCACTGTGGGCTTCTTGGCCGCG 358
QY 201 GlnProLeuGlnGluArgAlaGlnAlaThrPglyLeuArgLeuArgAlaArgMetGluGlu 220
Db 359 CAGCGCGCTACAGAGCGGGCCAGCGCTGGGGCGAGCGGTGCGCGCGGATGGAGGAG 418
QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 419 ATGGGAGCGGACCCCGGACCGCTGACAGAGTGAAGGAGCAGGTGGCGGAGGTGGCG 478
QY 241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 479 GCCAAGCTGGAGGAGCAGGCGCCAGCAGATACGCTGCAAGCGCGAGGCTTCCAGGCGCG 538
QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
```

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Db 539 CTCAGAGCTGTTTCAGCCCTGTGTGAAGACATGAGCGCACTGGGCCGGCTGGTG 598
QY 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAspHis 299
Db 599 GAGAAGGTGACGCTGCCGTGGGCACACAGCGCGCCCTGTGTGCCCGACCAATCAC 655

RESULT 9
US-10-211-689-35
; Sequence 35, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John II
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (sasha)
; APPLICANT: Khrastov, Nikolai V.
; APPLICANT: Lepley, Denise M.
; APPLICANT: MacDougall, John R.
; APPLICANT: Pena, Carol A.
; APPLICANT: Feyman, John A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Smithson, Richard A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO
; FILE REFERENCE: 21402-416B
; CURRENT APPLICATION NUMBER: US/10/211,689
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/311751
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/310,802
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,795
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/361,159
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/373,050
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/380,970
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/381,030
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/323,944
; PRIOR FILING DATE: 2001-09-21
; Remaining Prior Application data removed - See File wrapper or PALM.
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 35
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(718)
US-10-211-689-35

Alignment Scores:
Pred. No.: 2,91e-90 Length: 718
Score: 1026.00 Matches: 214
```

Percent Similarity: 71.6% Conservative: 0
Best Local Similarity: 71.6% Mismatches: 1
Query Match: 68.7% Indels: 84
DB: 4 Gaps: 1

US-09-827-854A-2 (1-299) x US-10-211-689-35 (1-718)

QY 1 LysValGluGlnAlaValAlaGluThrGluProGluProGluArgGlnThrGluTrp 20
DB 65 AAGTGGAGCAAGCGGTGGAGACAGACCGGAGCCGAGCTGCGCCAGACAGCCGAGTGG 124
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGluArgPheTrpAspTyrLeuArgTrpVal 40
DB 125 CAGAGCGCCGAGCGCTGGGAACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 184
QY 41 GlnThrLeuSerGluGlnValGlnGluGluLeuSerSerGlnValThrGlnGluLeu 60
DB 185 CAGACACTGTCTGAGCAGGTGGAGGAGGCTGCTCAGCTCCCAAGGTCCACCCAGGAAC 244
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
DB 245 AGGCGCTGATGACGAGACATGAGAGGTGAGGCTTACAAATCGGAACCTGGAGGAA 304
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
DB 305 CAACCTACCCCGGTGGCGGAGGAGACGCGGCGACGCTGTCCAAGGAG----- 352
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
DB 352 ----- 352
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
DB 352 ----- 352
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
DB 352 ----- 352
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
DB 352 ----- 352
QY 181 LeuGlyProLeuValGluGlnGlnArgValArgAlaAlaThrValGlySerLeuAlaGly 200
DB 353 CTGGGCCCCCTGGTGGACAGGCGCGCTGGCGGCCCACTGTGGCTTCTTGGCCGCG 412
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
DB 413 CAGCCGCTACAGAGCGGCGCCAGGCTGGCGGAGCGGCTGGCGCGCGGATGGAGGAG 472
QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
DB 473 ATGGGCGCGGACCCCGCCGACCCGCTGGACGAGGTGAAGGAGCAGGTGGCGGAGGTGCGC 532
QY 241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
DB 533 GCCAAGCTGGAGAGACAGGCGCCAGCAGATACGCTGCAGGCGCGAGGCTTCCAGGCCCGC 592
QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
DB 593 CTCAAGAGCTGGTTTCAGAGCCCTGGTGGAGAGACATGCAGCGCCAGTGGCGCGGCTGGTG 652
QY 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
DB 653 GAGAAGGTGAGGCTGCGGTGGGCACCGAGCGCCGCTGTGGCCCGCAATCAC 709

RESULT 10

US-10-211-689-31
; Sequence 31, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John II

QY 1 LysValGluGlnAlaValAlaGluThrGluProGluProGluArgGlnThrGluTrp 20
DB 72 AAGTGGAGCAAGCGGTGGAGACAGACCGGAGCCGAGCTGCGCCAGACAGCCGAGTGG 131
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
|||||

; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Baha A.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Khrantsov, Nikolai V.
; APPLICANT: Lepley, Denise M.
; APPLICANT: MacDougall, John R.
; APPLICANT: Pena, Carol A.
; APPLICANT: Peyman, John A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416B
; CURRENT APPLICATION NUMBER: US/10/211,689
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/311751
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/310,802
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,795
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/361,159
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/373,050
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/380,970
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/381,030
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/323,944
; PRIOR FILING DATE: 2001-09-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 31
; LENGTH: 802
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(716)
US-10-211-689-31

Alignment Scores:
Pred. No.: 3,37e-90 Length: 802
Score: 1026.00 Matches: 214
Percent Similarity: 71.6% Conservative: 0
Best Local Similarity: 71.6% Mismatches: 1
Query Match: 68.7% Indels: 84
DB: 4 Gaps: 1

US-09-827-854A-2 (1-299) x US-10-211-689-31 (1-802)

Db 132 CAGAGCGCCAGCGCTGGGAACCTGGCACCTGGGTGCGCTTTTGGGATTACCTGGCGTGGTG 191
Qy 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 192 CAGACACTCTGTAGCAGGTGAGAGGAGCTGCTCAGCTCCAGGTCCACCGAGGAACGT 251
Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu 80
Db 252 AGGCGCTGATGAGCAGACCATGAAGAGTTGAAGGCTCAAACTCGAACTGGAGGAA 311
Qy 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAla 100
Db 312 CAACTGACCCCGTGGCGAGGAGACGCGGCGCTGTCCAAGGAG----- 359
Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 359 ----- 359
Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 359 ----- 359
Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 359 ----- 359
Qy 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
Db 359 ----- 359
Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 360 CTGGGCGCCCTGTGTGAACAGAGCGCGCTGCGGCGCCCACTGTGGGCTTCTCTGGCGGC 419
Qy 201 GlnProLeuGlnGluArgAlaGlnAlaTyrGlyGluArgLeuArgAlaArgMetGluGlu 220
Db 420 CAGCCGCTACAGAGCGGCGCCAGCGCTGGGCGCGAGCGCTGCGCGCGGATGGAGGAG 479
Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 480 ATGGGACGCGGACCCCGACCGCCCTGGACGAGGTGAAGGACGAGGTGGCGGAGGTGGCG 539
Qy 241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 540 GCCAAGCTGGAGGAGCAGGCCAGCAGATACGCTGCAGCGCCGAGGCTTCCAGGCCCGC 599
Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db 600 CTCGAAGCTGGTTCTGAGCCCTGGTGGAAAGACATGCAGCGCCAGTGGCGCGGCTGGTG 659
Qy 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 660 GAGAAGTGCAGCTGCGGTGGGACACGAGCGCGCCCTGTGCCAGCGCAATCAC 716

RESULT 11
US-10-211-689-43
; Sequence 43, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
; APPLICANT: Alsebrook, John II
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine B.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Bena A.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Khrantsov, Nikolai V.
; APPLICANT: Lepley, Denise M.
; APPLICANT: McDougall, John R.
; APPLICANT: Pena, Carol A.
; APPLICANT: Peyman, John A.

Alignment Scores:
Pred. No.: 1,63e-87 Length: 652
Score: 997.00 Matches: 210
Percent Similarity: 70.2% Conservative: 0
Best Local Similarity: 70.2% Mismatches: 1
Query Match: 66.8% Indels: 88
DB: 4 Gaps: 1

US-09-827-854A-2 (1-299) x US-10-211-689-43 (1-652)

Qy 1 LysValGluGlnAlaValGluThrGluProGluLeuArgGlnGlnThrGluTrp 20
Db 11 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGAGCTGGCGCCAGCAGACCGAGTGG 70
Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 71 CAGAGCGCGCAGCGCTGGGAACCTGGGCACCTGGGTGCTTTTGGGATTACCTGGCTGGTG 130
Qy 41 GlnThrLeuSerGluGlnValGlnGluLeuSerSerGlnValThrGlnGluLeu 60
Db 131 CAGACACTGCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCAGGTCCACCGAGAACTG 190
Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu 80
Db 191 AGGCGCTGATGGACGAGACCATCAAGGAGTGTGAAGGCTTACAAATCGAACTGGAGGAA 250
Qy 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAla 100
Db 251 CAACTGACCCCGTGGCGAGGAGACCGCGGCGAGCTGTCCAAGGAGCTGCAGCGCGCG 310

; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shinkete, Richard A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416B
; CURRENT APPLICATION NUMBER: US/10/211,689
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/311751
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/310,802
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,795
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/361,159
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/373,050
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/380,970
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/381,030
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/323,944
; PRIOR FILING DATE: 2001-09-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: CuroSeqdist version 0.1
; SEQ ID NO 43
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(652)
; US-10-211-689-43

Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnThrArgGly 120
 Db 311 CAGGCCCGCTGGCGCGGACATGGAGACGTGCCCGCGCTGGTGCAGTACCGCGGC 370
 Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
 Db 371 GAGGTGCAGGCATGCTCGGCCAGACACCGAGGAGTGGGGTGGCTCGCTCCAC 430
 Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
 Db 431 CTGCGCAAGCTGCGTAAGCGCTCTCCGCGATGCCGATGAC----- 472
 Qy 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
 Db 472 ----- 472
 Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
 Db 472 ----- 472
 Qy 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
 Db 472 ----- 472
 Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
 Db 472 ----- 472
 Qy 241 AlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
 Db 473 -----CTGGAGGAGCAGCGCCAGCAGATACGCTGCAGCGGAGGCTTCAGGCGCGC 526
 Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
 Db 527 CTCAGAGCTGGTTCGAGCCCTGCTGGAGACATGTCAGCGCAGTGGCGCGGTGGTG 586
 Qy 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
 Db 587 GAGAAGGTGCAGGCTGCGTGGGCACCGCGCGCCCTGTGCCCCAGCACAATCAC 643

RESULT 12

US-10-211-689-41

; Sequence 41, Application US/10211689

; Patent No. 6974884

; GENERAL INFORMATION:

; APPLICANT: Alsobrook, John II

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gangolli, Esha A.

; APPLICANT: Gorman, Linda

; APPLICANT: Guo, Xiaojia (Sasha)

; APPLICANT: Khamstov, Nikolai V.

; APPLICANT: Lepley, Denise M.

; APPLICANT: MacDougall, John R.

; APPLICANT: Pena, Carol A.

; APPLICANT: Peyman, John A.

; APPLICANT: Patturajan, Meera

; APPLICANT: Rieger, Daniel K.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Smithson, Glennda

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Vernet, Corine A. M.

; APPLICANT: Voss, Edward Z.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-416B

; CURRENT APPLICATION NUMBER: US/10/211,689

; CURRENT FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: 60/311751

; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/310,802
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/310,795
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/311,292
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 60/361,159
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: 60/373,050
 ; PRIOR FILING DATE: 2002-04-16
 ; PRIOR APPLICATION NUMBER: 60/380,970
 ; PRIOR FILING DATE: 2002-05-15
 ; PRIOR APPLICATION NUMBER: 60/311,979
 ; PRIOR FILING DATE: 2001-08-13
 ; PRIOR APPLICATION NUMBER: 60/381,030
 ; PRIOR FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 60/323,944
 ; PRIOR FILING DATE: 2001-09-21
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 132
 ; SOFTWARE: Curaseq1ist version 0.1
 ; SEQ ID NO 41
 ; LENGTH: 709
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (2)..(709)
 ; US-10-211-689-41

Alignment Scores:
 Pred. No.: 1,82e-87 Length: 709
 Score: 997.00 Matches: 210
 Percent Similarity: 70.2% Conservative: 0
 Best Local Similarity: 70.2% Mismatches: 1
 Query Match: 66.8% Indels: 88
 DB: 4 Gaps: 1

US-09-827-854A-2 (1-299) x US-10-211-689-41 (1-709)

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 Db 68 AAGGTGGAGCAAGCGGTGGAGACAGAGCGGAGCGGAGCTGCCAGCAGACCGAGTGG 127
 Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
 Db 128 CAGAGCGCGCAGCGCTGGGAACCTGGGCTCGCTTTTGGGATTACCTGGCTGGGTG 187
 Qy 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
 Db 188 CAGACACTGTCTGAGCAGGTGTCAGAGGAGCTGCTCAGTCCAGGTCCAGGAACTG 247
 Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
 Db 248 AGGGCGCTGATGGACGAGACCATGAAGAGTTGAAGGCTTACAAATCGGAACCTGG 307
 Qy 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
 Db 308 CAACTGACCCCGTGGCGGAGAGACGCGGCGCTGTCTCAAGGAGCTGCAGCGCGCG 367
 Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
 Db 368 CAGGCGCGCTGGCGCGGACATGAGAGACGTGGCGCGCCCTGGTGGTACGTACCGCG 427
 Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
 Db 428 GAGGTGCAGGCCATGCTCGGCCAGACACCGAGGAGCTGGGGTGGCGCTCCCTCC 487
 Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
 Db 488 CTGCGCAAGCTGCGTAAGCGGCTCTCTCCGCGATGCCGATGAC----- 529

QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
 Db 529 -----
 QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
 Db 529 -----
 QY 201 GlnProLeuGlnArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
 Db 529 -----
 QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluInValAlaGluValArg 240
 Db 529 -----
 QY 241 AlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
 Db 530 -----CTGGAGGAGCAGGCCCGCCAGCATACGCTGCAGGCCGAGGCTTCCAGGCCCGC 583
 QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
 Db 584 CTCAGAGCTGGTTCAGGCCCTTGGTGGAGACATGCGAGCGCCAGTGGGCGCGGTGGTG 643
 QY 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
 Db 644 GAGAGGTCAGGCTGCCGTGGGACCAGCGCCGCTCTGCCCCAGCGACAATCAC 700

RESULT 13

US-10-211-689-33
 ; Sequence 33, Application US/10211689
 ; Patent No. 6974684
 ; GENERAL INFORMATION:
 ; APPLICANT: Alcobrook, John II
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Guo, Xiaojia (Sasha)
 ; APPLICANT: Khrantsov, Nikolai V.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Pena, Carol A.
 ; APPLICANT: Peyman, John A.
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Rieger, Daniel K.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Smithson, Glennda
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Vernet, Corine A. M.
 ; APPLICANT: Voss, Edward Z.
 ; APPLICANT: Zhong, Mei
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 ; FILE REFERENCE: 21402-416B
 ; CURRENT APPLICATION NUMBER: US/10/211,689
 ; CURRENT FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: 60/311,751
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/310,802
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/310,795
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/311,292
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 60/361,159
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: 60/373,050
 ; PRIOR FILING DATE: 2002-04-16
 ; PRIOR APPLICATION NUMBER: 60/380,970
 ; PRIOR FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: 60/311,979
 ; PRIOR FILING DATE: 2001-08-13
 ; PRIOR APPLICATION NUMBER: 60/381,030
 ; PRIOR FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 60/323,944
 ; PRIOR FILING DATE: 2001-09-21
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 132
 ; SOFTWARE: CuratSeqList version 0.1
 ; SEQ ID NO 33
 ; LENGTH: 788
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (18)..(704)
 ; US-10-211-689-33
 Alignment Scores:
 Pred. No.: 2,1e-87 Length: 788
 Score: 997.00 Matches: 210
 Percent Similarity: 70.2% Conservative: 0
 Best Local Similarity: 70.2% Mismatches: 1
 Query Match: 66.8% Indels: 88
 DB: 4 Gaps: 1
 US-09-827-854A-2 (1-299) x US-10-211-689-33 (1-788)

QY 1 LysValGlnAlaValGluThrGluProGluProGluLeuArgGlnThrGluTrp 20
 Db 72 AAGGTGGAGCAGCGGTGGAGACAGAGCCGAGCCGAGCTGCCAGCAGACCGAGTGG 131
 QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
 Db 132 CAGAGCGCCAGCGCTGGGAACTGGCACTGGTGGTCTTTGGGATTACCTGGCTGGTG 191
 QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuLeuSerSerGlnValThrGlnGluLeu 60
 Db 192 CAGACACTGTCTCAGCAGGTGCAGAGGAGCTGCTCAGCTCCAGGTCACCCAGGAATG 251
 QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
 Db 252 AGGGCGCTGATGACGAGACCATGAAGAGTGAAGCCCTACAAATCGGAATCGAGGAA 311
 QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
 Db 312 CAACTGACCCCGTGGCGGAGGAGACGCGCGCACGGCTGTCCAAGGAGTGCAGCGCGC 371
 QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
 Db 372 CAGGCCCGCTGGCGCGGACATGAGGAGCGTGGCGCGCCCTGGTGCAGTACCGCGGC 431
 QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
 Db 432 GAGGTGAGGCCCATGCTCGGCCAGAGCAGCAGAGCTGGGTGGCTGCCCTCCCTCCAC 491
 QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
 Db 492 CTGGCAAGCTGCGTAAGCGGCTCTCCCGCATGCCGATGATGAC----- 533
 QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
 Db 533 -----
 QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
 Db 533 -----
 QY 201 GlnProLeuGlnArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
 Db 533 -----
 QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluInValAlaGluValArg 240

Db 533 ----- 533
Qy 241 AlalysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 534 -----CTGGAGGAGCAGGCCAGCAGATACCGCTGCAGGCCGAGGCTTCAGGCCGC 587
Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db 588 CTCAGAGCTGTTGAGGCCCTGGTGAAGACATGACGCCAGTGGGCCCGGCTGGTG 647
Qy 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 648 GAGAGGTGCGAGCTGCGGTGGGCACAGCGCGCCCTGTGCCCAGCGACAATCAC 704

RESULT 14

US-08-949-155-51
; Sequence 51, Application US/08949155
; Patent No. 6271436
; GENERAL INFORMATION:
; APPLICANT: Piedrahita, Jorge A
; APPLICANT: Bazer, Fuller W
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Generation of Transgenic Animal Species
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE AND DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,155
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,338
; FILING DATE: 11-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/046,094
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hibler, David W.
; REGISTRATION NUMBER: 41,071
; REFERENCE/DOCKET NUMBER: TANK:177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4267 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-949-155-51

Alignment Scores:
Pred. No.: 6,07e-86 Length: 4267
Score: 992.00 Matches: 212
Percent Similarity: 59.9% Conservative: 40
Best Local Similarity: 50.4% Mismatches: 40
Query Match: 66.4% Indels: 130
DB: 3 Gaps: 3

US-09-827-854A-2 (1-299) x US-08-949-155-51 (1-4267)

Qy 7 GluThrGluProGluProGluLeuArg-----GlnGlnThrGluTrpGlnSerGly 23

Db 2490 GAGCCGGGGCGCGCGCGGAGGTGCACGTGTGTGGGAGGAGCCCAAGTGCAGGGCAGC 2549
Qy 24 GlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpValGlnThrLeu 43
Db 2550 CAGCCCTGGGAGCAGGCCCTCTGGCGCTTCTGGGATTAACCTGCGCTGGGTGAGTCCCTG 2609
Qy 44 SerGluGlnValGlnGluLeuSerSerGlnValThrGlnGluLeu----- 60
Db 2610 TCTGACCAGTGTGAGGAGGAGCTGCTCAGCACCAAGGTCAACCCAGGAACACT-GACGTAAGT 2668
Qy 60 ----- 60
Db 2669 GCCCACCCGACTCCCGCGCGCGCGCGCGCGCGCTGACCCCTCTCTGGCGA 2728
Qy 60 ----- 60
Db 2729 ACCGTGTGTCTTGAGACCTCAGGCTCCACCGCTCCGGGTTCCTTCTGTCTCTGTGCGCA 2788
Qy 60 ----- 60
Db 2789 ACTCTGGGGGTCTGGGTCTCTGTTCTTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2848
Qy 60 ----- 60
Db 2849 AACTTTTTCTTTTTCTTTTCATTGACTTCATGCTTGTCTTCTTCTTCTTCTTCTTCTTCT 2908
Qy 60 ----- 60
Db 2909 TGCCTTCGCTCTCTCTGGGTCAGTCTTGCGGTCTCTTGTCTCTCTCTCTCTCTCTCTCT 2968
Qy 60 ----- 60
Db 2969 GTCTGTGCCATCGCCAGCTCAGGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3028
Qy 61 -----ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeu 78
Db 3029 CGGCCAGGAGCTGTAGAGGAGCATGAAGGAGGTGAAGGCTTACCGGAGGAGCTG 3088
Qy 79 GluGluGlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGln 98
Db 3089 GAGCGCAGCTGGGCCCCCTGACCCAGGAGCAGCGCGCGCTGTCCAAGGAGCTGCAG 3148
Qy 99 AlaAlaGlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyr 118
Db 3149 CGCGCGCAGGCCCGCTGGCGCGCATGAGAGACGTGCGCAACCGCTTGGTCTCTTAC 3208
Qy 119 ArgGlyGluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAla 138
Db 3209 CGCAGCGAGGTGCACACATGTTGGGCCAGACCCAGGAGCTGCGGAGCGCTGGCT 3268
Qy 139 SerHisLeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArg 158
Db 3269 TCCACCTGCGCAAGCTGCGCAAGCGCTGCTCCGCGACACCGAGGACCTCAGAGAAGCG 3328
Qy 159 LeuAlaValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaTyr 178
Db 3329 CTGGCCGTGTACAGCGCGGCTGCGCGAGGCGCGCGAGCGCGCGCTGAGGAGCGCTCCGC 3388
Qy 179 GluArgLeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeu 198
Db 3389 GAGCGCTCGGGCCCTGTTGGAGCAGGCGCGATTGCGCGCGCCACCTGAGTACCAGG 3448
Qy 199 AlaGlyGlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMet 218
Db 3449 GCCCGCAGCGCTGCGCGAGCGCGAGAGCTTGGGGCCAGAAAGCTGCGCGAGCGGCTG 3508
Qy 219 GluGluMetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGlu 238
Db 3509 GAGGAGATGGGAGCGCGACCCGCGACCGCTGTGATGATGCTGAGCTGAGCTGAGGAG 3568
Qy 239 ValArgAlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGln 258

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GenCore version 5.1.9
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Perfect score: 1493

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	1493	100.0	1147	7	US-10-257-021-63 Sequence 63, Appl

2	1493	100.0	1156	3	US-09-827-854-8	Sequence 8, Appli
3	1493	100.0	1156	3	US-09-870-759-129	Sequence 129, App
4	1493	100.0	1156	3	US-09-802-640-17	Sequence 17, Appl
5	1493	100.0	1156	3	US-09-751-708A-129	Sequence 129, App
6	1493	100.0	1156	7	US-10-301-822-5	Sequence 5, Appli
7	1493	100.0	1156	7	US-10-313-641-1	Sequence 1, Appli
8	1493	100.0	1156	7	US-10-403-902A-17	Sequence 17, Appli
9	1493	100.0	1156	7	US-10-428-551-1	Sequence 1007, Ap
10	1493	100.0	1156	8	US-10-641-643-1007	Sequence 125, App
11	1493	100.0	1156	9	US-10-428-817A-125	Sequence 1, Appli
12	1493	100.0	1156	9	US-10-794-198A-1	Sequence 10, Appl
13	1493	100.0	1156	10	US-10-852-335A-10	Sequence 106, App
14	1493	100.0	1156	10	US-10-937-758A-106	Sequence 63, Appl
15	1493	100.0	1156	10	US-10-773-446-63	Sequence 5, Appli
16	1493	100.0	1156	15	US-11-186-284-5	Sequence 1, Appli
17	1493	100.0	1156	15	US-11-055-309A-1	Sequence 34, Appl
18	1493	100.0	1186	10	US-10-929-182-34	Sequence 246, App
19	1493	100.0	1291	3	US-09-919-039-246	Sequence 454, App
20	1493	100.0	1291	6	US-10-044-090-454	Sequence 256, App
21	1493	100.0	1291	6	US-10-116-802-256	Sequence 8338, Ap
22	1493	100.0	1428	9	US-10-723-860-8338	Sequence 12, Appli
23	1489	99.7	1156	3	US-09-827-854-12	Sequence 9, Appli
24	1485	99.5	1156	3	US-09-827-854-9	Sequence 11, Appl
25	1485	99.5	1156	3	US-09-827-854-11	Sequence 760, App
26	1484	99.4	1157	3	US-09-954-456-760	Sequence 2244, Ap
27	1484	99.4	1157	3	US-09-880-107-2244	Sequence 655, App
28	1484	99.4	1157	3	US-09-960-706-655	Sequence 409, App
29	1484	99.4	1157	3	US-09-873-319-409	Sequence 3, Appli
30	1484	99.4	1157	7	US-10-313-641-3	Sequence 3, Appli
31	1484	99.4	1157	7	US-10-428-551-3	Sequence 1291, Ap
32	1484	99.4	1157	8	US-10-240-425-1291	Sequence 4536, Ap
33	1484	99.4	1157	9	US-10-723-860-4536	Sequence 3, Appli
34	1484	99.4	1157	9	US-10-794-198A-3	Sequence 3787, Ap
35	1484	99.4	1157	10	US-10-843-641A-3787	Sequence 3, Appli
36	1484	99.4	1157	15	US-11-055-309A-3	Sequence 7, Appli
37	1481	99.2	1156	3	US-09-827-854-7	Sequence 126, App
38	1480	99.1	1220	16	US-11-091-883-126	Sequence 104, App
39	1480	99.1	1497	7	US-09-971-392-104	Sequence 265, App
40	1480	99.1	1497	7	US-10-252-152-265	Sequence 10, Appl
41	1478	99.0	1156	3	US-09-827-854-10	Sequence 475, App
42	1465	98.1	1372	9	US-10-741-600-475	Sequence 3, Appli
43	1389.5	93.1	1279	7	US-10-291-265-3	Sequence 3, Appli
44	1389.5	93.1	1279	15	US-11-000-463-3	Sequence 154, App
45	1378	92.3	1372	8	US-10-741-601-154	

ALIGNMENTS

RESULT 1
US-10-257-021-63
; Sequence 63, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.036902
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 1147
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-021-63

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Alignment Scores:
Pred. No.: 9,69e-135 Length: 1147
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-827-854A-2 (1-299) x US-10-257-021-63 (1-1147)

QY 1 LyeValGluGlnAlaValGluThrGluProGluLeuArgGlnGlnThrGluTrp 20
Db 100 AAGGTGAGCAACGGTGGAGACAGCCGAGCCGAGCTGCGCCAGACAGCCGAGTGG 159
QY 21 GinSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 160 CAGAGCGCCGACGCTGGGAACCTGGCACCTGGTTCGCTTTGGGATTACCTGGCTGGGTG 219
QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 220 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGCTCCAGGTCACCCAGGAACCTG 279
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 280 AGGCGCGCTGATGACGAGACCATGAAGGAGTTGAAGCCCTACAAATCGGAACCTGGAGGA 339
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaLeuLeuSerLysGluLeuGlnAlaAla 100
Db 340 CAACTGACCCGCTGGCGAGGAGACGCGGCACGCTGTCCAAGGAGCTGCAGGCGGCG 399
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 400 CAGGCGCGCTGGCGCGACATGGAGGAGCTGTGGCGCGCTGTGTGAGTACCGCGGC 459
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 460 GAGGTGAGGCCATGCTCGGCCAGAGACCGAGAGCTGGGGTGGCGCTCCGCTCCAC 519
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 520 CTGCGCAAGCTGGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAGCGCTGGCA 579
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaLeuArgGluArg 180
Db 580 GTGTACAGCGCGCGCGCGAGGCGCGAGCGCGCTCAGCGCCATCCCGAGCGC 639
QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 640 CTGGGGCCCCCTGGTGAACAGGGCGCGTGGGGCGCGCCACTGTGGGCTCCCTGGCGCGC 699
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
Db 700 CAGCCGCTACAGAGCGGGCCAGGCTGGGGCGAGCGGCTGCGCGCGGATGGAGGAG 759
QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 760 ATGGGAGCGGACCGCGACCGCTGGACGAGGTGAAGGAGCAGGTGGCGGAGTGGCGC 819
QY 241 AlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 820 GCCAAGCTGAGGAGGAGGCGCCAGCAGATACGCTTGAGGCCGAGGCTTCCAGGGCCCGC 879
QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db 880 CTCAGAGCTGGTTCGAGCCCTGGTGAAGACATGCAGCGCCAGTGGGCGGGCTGGT 939
QY 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 940 GAGAGGTGAGGCTGCGTGGGACCCAGCGCGCGCCCTGTGCGCCAGCGCAATCAC 996

RESULT 2
US-09-827-854-8
; Sequence 8, Application US/09827854

; Patent No. US20020123093A1
; GENERAL INFORMATION:
; APPLICANT: Zannis, Vassilis
; APPLICANT: Kypros, Kyriakos E.
; TITLE OF INVENTION: Compounds and methods for lowering
; TITLE OF INVENTION: cholesterol levels without inducing hypertriglyceridemia
; FILE REFERENCE: 07180/004003
; CURRENT APPLICATION NUMBER: US/09/827,854
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/679,088
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 09/544,386
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-854-8

Alignment Scores:
Pred. No.: 9,78e-135 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-2 (1-299) x US-09-827-854-8 (1-1156)

QY 1 LyeValGluGlnAlaValGluThrGluProGluLeuArgGlnGlnThrGluTrp 20
Db 115 AAGGTGAGCAACGGTGGAGACAGAGCCGAGCCGAGCTGCGCCAGACAGCCGAGTGG 174
QY 21 GinSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 175 CAGAGCGCGCAGCGCTGGGAACCTGGCACCTGGTTCGCTTTGGGATTACCTGGCGCTGGGTG 234
QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 235 CAGACACTGTCTGAGCAGGTGCAGGAGGAGCTGCTCAGTCCAGGTCACCCAGGAACCTG 294
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 295 AGGCGCTGATGACGAGACCATGAAGGAGTTGAAGGCCCTACAAATCGGAACCTGGAGAA 354
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db 355 CAACTGACCCGCTGGCGAGGAGACGCGGGCACGCTGTCCAAGGAGCTGCAGGCGGCG 414
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 415 CAGCGCGCGCTGGCGCGGACATGAGGAGCTGTGGCGCGCTGTGTGAGTACCGCGCGC 474
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 475 GAGGTGAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGGCGGTGGCGCTCGCTCCCGCCAC 534
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 535 CTCGCAAGCTGGCTAAGCGGCTCTCCCGCGATGCCGATACCTGCAGAGCGGCTGGCA 594
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaLeuArgGluArg 180
Db 595 GTGTACAGCGCGGCGCGCGGAGGCGCGAGCGCGGCTCAGCGCCATCCCGAGCGC 654
QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 655 CTGGGCGCCCTGGTGGAAACAGGCGCGCTGCGGGCGCGCCACTGTGGGCTCCCTGGCGCGC 714
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuAlaArgMetGluGlu 220
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Db 715 CAGCCGCTACAGGAGCGGGCCAGCGCTGGGGCGAGCGCTGCGCGCGAGTGGAGGAG 774
QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 775 ATGGCAGCCGACCCCGGACCGCTGGACGAGTGAAGGAGCAGAGTGGCGAGGTGCGC 834
QY 241 AlaLysLeuGluGlnAlaGlnGlnInleAArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 835 GCCAAGCTGGAGGAGCAGGCCAGCAGATAGCCCTGCAGCGCAGGCTTCCAGGCCCGC 894
QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db 895 CTCAGAGCTGGTTCGAGCGCCCTGGTGAAGACATGACAGCGCCAGTGGCGCGGCTGGTG 954
QY 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 955 GAGAGGTGAGCTGCGTGGGACCGCGCGCCCTGTGGCCCGCAATCAC 1011
RESULT 3
US-09-870-759-129
; Sequence 129, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(1014)
; OTHER INFORMATION:
US-09-870-759-129
Alignment Scores:
Pred. No.: 9,78e-135 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-09-827-854A-2 (1-299) x US-09-870-759-129 (1-1156)
QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
Db 115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGCGAGCTGCGCCAGCAGACCGAGTGG 174
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 175 CAGAGCGCCGACGCTGGGAACCTGGCACTGGGTGCTTTGGGATTACCTGCGCTGGGTG 234
QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 235 CAGACACTGCTGAGCAGAGTGGAGGAGGAGCTGCTCAGCTCCAGGTGCACCCAGGAATG 294
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 295 AGGCGCTGATGACGACCATGAGAGACTTGAAGCCTACAAATCGGAATGGAGAA 354
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db 355 CAACCTGACCCCGTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGCGCGC 414
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120

Db 415 CAGCCCGCTGGCGCGGACATGGAGGACGTGTGCGCGCCCTGTGTGCAGTACCGCGC 474
QY 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 475 GAGGTGAGGCCCATGTCTCGGCCAGAGCACGAGAGAGTGGGGTGCCTCGCTCCAC 534
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 535 CTGGCAGCTGGTAAAGCGCTCTCTCCGCGATGCCGATGACCTGCAGAGGCGCTGGCA 594
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaAlaArgGluArg 180
Db 595 GTGTACAGCGCGGGCGCGAGGGCGCGAGCGCGCTCAGCGGCATCCCGGAGCGC 654
QY 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 655 CTGGGCGCCCTGTGTGAACAGGGCGCGCTGCGGGCGCCACTGTGGGCTCCCTGGCGCGC 714
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
Db 715 CAGCCGCTACAGAGCGGGCCAGGCCCTGGGGCGAGCGGTGCGCGCGCGATGGAGAG 774
QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 775 ATGGCAGCGCGACCCCGCGAGCTGGACGAGGTGAAGGAGCAGAGTGGCGAGGTGCGC 834
QY 241 AlaLysLeuGluGlnAlaGlnGlnInleAArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 835 GCCAAGCTGGAGGAGCAGGCCAGCAGATACGCTGCAGGCCGCGAGGCTTCCAGGCCCGC 894
QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db 895 CTCAGAGCTGGTTCGAGCCCTGGTGAAGACATGCGAGCCCATGCGCGCGCGCTGGTG 954
QY 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 955 GAGAGGTGAGGCTGCGGTGGCCAGCGCGCCCTGTGTGCCCGGACATCAC 1011
RESULT 4
US-09-802-640-17
; Sequence 17, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsai Aruna
; APPLICANT: Kleyen Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(1014)
; OTHER INFORMATION: Nucleotide Sequence encoding apolipoprotein E
; OTHER INFORMATION: (APOE)
US-09-802-640-17
Alignment Scores:
Pred. No.: 9,78e-135 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

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US-09-827-854A-2 (1-299) x US-09-802-640-17 (1-1156)
QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
DB 115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGAGCCGAGCTGGCCAGCAGACCGAGTGG 174
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
DB 175 CAGAGCGGCGAGCGTGGGAACCTGGCACTGGGTGCTTTGGGATTACCTGGCGTGGGTG 234
QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
DB 235 CAGACACTGCTGTGAGCAGGTGGAGAGAGCTGCTCAGCTCCAGGTCCACCGAGAACTG 294
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu 80
DB 295 AGGCGCGCTGATGGAGAGACCATGAAGAGATTGAAGCCCTCAAAATCGGAATCGGAGAA 354
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAla 100
DB 355 CAACCTGACCCCGTGGCGGAGAGACCGCGGACGCGCTGTCCAAGAGAGCTGCAGGCGGCG 414
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
DB 415 CAGGCGCGGCTGGCGCGGACATGGAGGAGTGAAGGCTTGAAGGCTCAAAATCGGAATCGGAGAA 354
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
DB 595 GTGTACAGCGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 654
QY 181 LeuGlyValGlnAlaValGlyThrSerAlaAlaProValProSerAspAenHis 299
DB 955 GAGAAGGTGAGGCTGCGGTGGGACACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1011

RESULT 5
US-09-751-708A-129
; Sequence 129, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371

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; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(1014)
; OTHER INFORMATION:
US-09-751-708A-129

Alignment Scores:
Pred. No.: 9,78e-135 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-2 (1-299) x US-09-751-708A-129 (1-1156)
QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp 20
DB 115 AAGGTGGAGCAAGCGGTGGAGACAGAGCCGAGCCGAGCTGGCCAGCAGACCGAGTGG 174
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
DB 175 CAGAGCGGCGAGCGTGGGAACCTGGCACTGGGTGCTTTGGGATTACCTGGCGTGGGTG 234
QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
DB 235 CAGACACTGCTGTGAGCAGGTGGAGAGAGTGTCTCAGCTCCAGGTCCACCGAGAACTG 294
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu 80
DB 295 AGGCGCGCTGATGGAGAGACCATGAAGGAGTGAAGGCTTGAAGGCTCAAAATCGGAATCGGAGAA 354
QY 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAla 100
DB 355 CAACCTGACCCCGTGGCGGAGAGACCGCGGACGCGCTGTCCAAGAGAGCTGCAGGCGGCG 414
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
DB 415 CAGGCGCGGCTGGCGCGGACATGGAGGAGTGAAGGCTTGAAGGCTCAAAATCGGAATCGGAGAA 354
QY 121 GlnValGlnAlaMetLeuGlyGlnSerThrGluLeuArgValArgLeuAlaSerHis 140
DB 475 GAGGTGCAGGCCATGCTCGGCCAGAGACCGAGGAGCTGCGGTGCGCTCCCTCCAC 534
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
DB 535 CTGCGGCAAGCTGGTGAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAAGCGCTGGCA 594
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg 180
DB 595 GTGTACAGCGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 654
QY 181 LeuGlyProLeuValGlnGluArgValArgAlaAlaThrValGlySerLeuAlaGly 200
DB 655 CTGGGCGCGCTGGTGAACAGGCGCGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 714
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTrpGlyValArgLeuArgAlaArgMetGluGlu 220
DB 715 CAGCGCGCTACAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 774
QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
DB 775 ATGGGCGAGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 834
QY 241 AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260

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Db      835  GCCAAGCTGGAGGAGCAGGCCAGACATACGCTCGAGGCCGAGGCTTCCAGGCCCGC 894
Qy      261  LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db      895  CTCGAAGAGCTGGTTCGAGCCCTCGTGGAGACATGACAGGCCAGTGGCGCGGCTGGTG 954
Qy      281  GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db      955  GAGAGAGTGCAGGCTGCGGTGGGACACAGGCCCGCCCTGTGCCAGGACATCAC 1011

RESULT 6
US-10-301-822-5
; Sequence 5, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burt, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P28NM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)...(1014)
US-10-301-822-5

Alignment Scores:
Pred. No.:          9,78e-135          Length: 1156
Score:             1493.00           Matches: 299
Percent Similarity: 100.0%           Conservative: 0
Best Local Similarity: 100.0%         Mismatches: 0
Query Match:       100.0%             Indels: 0
DB:                7                 Gaps: 0

US-09-827-854A-2 (1-299) x US-10-301-822-5 (1-1156)

Qy      1  LysValGluGlnAlaValGluThrGluProGluLeuArgGlnGlnThrGluTrp 20
Db      115  AAGGTGAGCAAGCGGTGGAGACAGAGCCGAGCGAGCTGCCAGCAGCAGACCGAGTGG 174
Qy      21  GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db      175  CAGAGCGCCAGCCGCTGGGAACCTGGCACTGGGTGCTTTTGGGATTTACCTGCGCTGGTG 234
Qy      41  GlnThrLeuSerGluGlnValGlnGluLeuSerSerGlnValThrGlnGluLeu 60
Db      235  CAGACACTGTCTGAGCAGGTGCAGGAGAGCTGCTCAGTCCAGGTCCACCCAGGAACCTG 294
Qy      61  ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db      295  AGGCGCTGTATGGACGAGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACCTGGAGAA 354
Qy      81  GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
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Db      355  CAACTGACCCGGTGGCGGAGAGACCGCGGCACGGCTGTCCAGAGAGCTGCAGCGCGCG 414
Qy      101  GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTrpArgGly 120
Db      415  CAGCCCGGCTGGCGCGGACATGGAGAGACGTGTGCGCGCCGCTGGTGCAGTACCGCGGC 474
Qy      121  GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db      475  GAGGTGAGGCCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGTGCGGCTGCCCTCCAC 534
Qy      141  LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db      535  CTGCGCAAGCTGCGTAAGCGCTCTCCGCGATGCCGATGACCTGCAGAGCGCTGCGCA 594
Qy      161  ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaAlaArgGluArg 180
Db      595  GTGTACCAAGCGCGGCCCGCGAGGGCGCGAGCGCGCTTCAGCGGCATCCGCGAGCGC 654
Qy      181  LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db      655  CTGGGGCCCTGTGTGGAAACAGGGCGCGGTGGCGGCGAGCGCTGCGCGCGATGGAGGAG 714
Qy      201  GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu 220
Db      715  CAGCGCGCTACAGGAGCGGCCCGCGAGCGCTGCGCGCGAGCGCTGCGCGCGATGGAGGAG 774
Qy      221  MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db      775  ATGGCGAGCGCGACCCCGCGAGCGCTGAGGAGGTGAAGGAGCAGGTGGCGGAGTGGCGC 834
Qy      241  AlaLysLeuGluGlnGlnAlaGlnGlnLeuArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db      835  GCCAAGCTGAGGAGAGCAGGCCCGCGAGTACGCTTCAGGCCGAGGCGCTTCAGGCCCGC 894
Qy      261  LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal 280
Db      895  CTCGAAGAGCTGGTTCGAGGCCCTGGTGGAAAGACATGCAGCGCCAGTGGCGCGGCTGGT 954
Qy      281  GluLysValGlnAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db      955  GAGAGAGTGCAGGCTGCGGTGGGACACCGCGGCCCGCTGTGCCAGGACATCAC 1011

RESULT 7
US-10-313-641-1
; Sequence 1, Application US/10313641
; Publication No. US20030162758A1
; GENERAL INFORMATION:
; APPLICANT: Ishida, Brian
; APPLICANT: Duncan, Keith
; APPLICANT: Bailey, Kathy
; APPLICANT: Kane, John
; APPLICANT: Schwartz, Daniel
; TITLE OF INVENTION: Treatments for Age Related-Macular Degeneration (AMD)
; FILE REFERENCE: P02351US2
; CURRENT APPLICATION NUMBER: US/10/313,641
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/415,864
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: US 60/340,498
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Human
US-10-313-641-1

Alignment Scores:
Pred. No.:          9,78e-135          Length: 1156
Score:             1493.00           Matches: 299
Percent Similarity: 100.0%           Conservative: 0
```

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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-827-854A-2 (1-299) x US-10-313-641-1 (1-1156)

QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnThrGluTrp 20
Db 115 AAGGTGAGCAAGCGGTGGAGACAGAGCCGAGCGAGCTGCGCCAGCAGACCGAGTGG 174
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 175 CAGAGCGCGCAGCGCTGGAACTGGCACTGGGTGCTTTGGATTACCTGCGCTGGGTG 234
QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 235 CAGACACTGTCTGAGCAGGTGGAGGAGCTGCTCAGCTCCAGGTACCCAGGAACTG 294
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu 80
Db 295 AGGGCGCTGATGACGAGACCATGAAGGAGTTGAAGGCTTACAAATCGGAACCTGGAGAA 354
QY 81 GlnLeuThrProValAlaGluThrArgAlaArgLeuSerLysGluLeuGlnAla 100
Db 355 CAACTGACCCCGGTGGCGGAGAGACGCGGCGCAGGCTGTCCAAGGAGCTGCGCGCGG 414
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 415 CAGGCCCGCTGGCGCGGACATGAGGAGCTGTGGCGCGCTGTGTGACAGTACCGCGGC 474
QY 121 GlnValGlnAlaMetLeuGlnSerThrGluLeuArgValArgLeuAlaSerHis 140
Db 475 GAGGTGACGAGCCATGCTCGGCCAGAGCACCGAGGAGCTGGCGGCTGTGTGACGTACCGGCG 534
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 535 CTGCGCAAGCTGGTGAAGCGGCTCTCCGCGATGCGGATGACCTGCAGAGCGCGCTGGCA 594
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgLysLeuSerAlaLeuArgGluArg 180
Db 595 GTGTACAGCCCGGCGCGCGGCGCGCGCGCGCTCAGCGGCTCAGCGGCTCAGCGGAGCG 654
QY 181 LeuGlyProLeuValGluGlnArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 655 CTGGGCGCGCTGGTGAAGCGCGCGCTGCGGCGCGCGCTGTGGGCTCCCTGGCGCGC 714
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTyrGluArgLeuArgAlaArgMetGluGlu 220
Db 715 CAGCCGCTACAGAGCGCGCGCGCGCGCGCGCTGGCGGAGCGGCTGCGCGCGGATGGAGGAG 774
QY 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 775 ATGGCGAGCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 834
QY 241 AlaLysLeuGluGlnAlaGlnGlnInileArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 835 GCCAAGCTGGAGGAGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 894
QY 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnThrAlaGlyLeuVal 280
Db 895 CTAAGAGCTGGTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 954
QY 281 GlnLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 955 GAGNAGGTGACAGCTGCGTGGGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1011

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RESULT 8

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US-10-403-902A-17
; Sequence 17, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bansal, Aruna

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; APPLICANT: Klynn, Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048B
; CURRENT APPLICATION NUMBER: US/10/403,902A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/802,640
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)...(1014)
; OTHER INFORMATION: Nucleotide Sequence encoding apolipoprotein E
; OTHER INFORMATION: (APOE)
US-10-403-902A-17

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Alignment Scores:
Pred. No.: 9,78e-135 Length: 1156
Score: 1493.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

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US-09-827-854A-2 (1-299) x US-10-403-902A-17 (1-1156)

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QY 1 LysValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnThrGluTrp 20
Db 115 AAGGTGAGCAAGCGGTGGAGACAGAGCCGAGCGCGAGCTGCGCCAGCAGACCGAGTGG 174
QY 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 175 CAGAGCGCGCAGCGCTGGAACTGGCACTGGGTGCTTTGGATTACCTGCGCTGGGTG 234
QY 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 235 CAGACACTGTCTGAGCAGGTGGAGGAGCTGCTCAGCTCCAGGTACCCAGGAACTG 294
QY 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGlu 80
Db 295 AGGGCGCTGATGACGAGACCATGAAGGAGTTGAAGGCTTACAAATCGGAACCTGGAGAA 354
QY 81 GlnLeuThrProValAlaGluThrArgAlaArgLeuSerLysGluLeuGlnAla 100
Db 355 CAACTGACCCCGGTGGCGGAGAGACGCGGCGCAGGCTGTCCAAGGAGCTGCGAGGCGG 414
QY 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 415 CAGGCCCGCTGGCGCGGACATGAGGAGCTGTGGCGCGCTGTGTGACAGTACCGCGGC 474
QY 121 GlnValGlnAlaMetLeuGlnSerThrGluLeuArgValArgLeuAlaSerHis 140
Db 475 GAGGTGACGAGCCATGCTCGGCCAGAGCACCGAGGAGCTGGCGGCTGTGTGACGTACCGGCG 534
QY 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspAspLeuGlnLysArgLeuAla 160
Db 535 CTGCGCAAGCTGGTGAAGCGGCTCTCCGCGATGCGGATGACCTGCAGAGCGCGCTGGCA 594
QY 161 ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgLysLeuSerAlaLeuArgGluArg 180
Db 595 GTGTACAGCCCGGCGCGCGGCGCGCGCGCGCTCAGCGGCTCAGCGGCTCAGCGGAGCG 654
QY 181 LeuGlyProLeuValGluGlnArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 655 CTGGGCGCGCTGGTGAAGCGCGCGCTGCGGCGCGCGCTGTGGGCTCCCTGGCGCGC 714
QY 201 GlnProLeuGlnGluArgAlaGlnAlaTyrGluArgLeuArgAlaArgMetGluGlu 220

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Db 295 AGGCGCTGATGGACGACACCATGAAGGAGTTGAAGGCTTACAAATCGGAACCTGAGGAA 354
Qy 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db 355 CAACGTGACCCCGGTGGCGGAGACGCGGCGACGGCTGTCCAAGGAGCTCGAGCGCGC 414
Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 415 CAGGCCCGCTGGCGCGGACATGGAGACGCTGTGGCGCCGCTGTGTGAGTACCGCGGC 474
Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 475 GAGGTGCGGACCATGCTCGGCGCAGACCGAGGAGCTGCGGCTGCGCTCCCTCCAC 534
Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
Db 535 CTGGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGCCGATGCCGATGCCG 594
Qy 161 ValTyrGlnAlaGlyAlaArgGluGluValAlaGluArgGlyLeuSerAlaIleArgGluArg 180
Db 595 GTGTACCAAGCGCGGCGCGCGAGGCGCGGCGCGGCGCTCAGCGCCATCCGCGAGCGC 654
Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 655 CTGGGCGCCCTGTGGTGGAAACAGGCGCGCTCGGCGGAGAGTGGCGGCGGATGGAG 714
Qy 201 GlnProLeuGlnAlaGlnAlaThrGlyGluArgLeuArgAlaArgMetGluGlu 220
Db 715 CAGCCGCTACAGAGCGGCGCCAGGCTGTGGCGAGCGGCTGTGGCGCGGATGGAGAG 774
Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 775 ATGGCAGCGCGGACCCGCGACCGCTTGGACGAGGTGAAGGAGCAGGTGGCGAGGTGGC 834
Qy 241 AlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 835 GCCAAGCTGGAGGAGCAGGCGCCAGCATACGCTGCGAGGCGGAGGCTTCCAGGCGCGC 894
Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTyrAlaGlyLeuVal 280
Db 895 CTCGAAGCTGGTTCTGAGGCCCTGTGTGAAGACATGACGCGCCAGTGGCGCGGCTGGT 954
Qy 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 955 GAGAGGTGCAGGCTGCCGTGGGCGACCGAGCGCGCCCTGTGCCCGGACCAATCAC 1011

RESULT 12
US-10-794-198A-1
; Sequence 1, Application US/10794198A
; Publication No. US2004026663A1
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Daniel
; APPLICANT: Duncan, Keith
; APPLICANT: Bailey, Kathy
; APPLICANT: Kane, John
; APPLICANT: Iehida, Brian
; TITLE OF INVENTION: METHODS TO INCREASE REVERSE CHOLESTEROL TRANSPORT IN THE RETINAL
; FILE REFERENCE: HO-P02351USA
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US/10794,198A
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 10/428,551
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/340,498
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/415,864
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1156
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; TYPE: DNA
; ORGANISM: HUMAN
US-10-794-198A-1
Alignment Scores:
Pred. No.: 9,78e-135 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0
US-09-827-854a-2 (1-299) x US-10-794-198A-1 (1-1156)
Qy 1 LysValGluGlnAlaValAlaGluThrGluProGluProGluLeuArgGlnGlnThrCluTrp 20
Db 115 AAGGTGAGGCAAGCGGTGGAGACAGAGCCGAGGCCGAGCTGCGCGACAGACACCGAGTGG 174
Qy 21 GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal 40
Db 175 CAGAGCGCGCAGCGCTGGGAACCTGGCACTGGGTGCTTTTGGGATTACCTGCGCTGGGTG 234
Qy 41 GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu 60
Db 235 CAGACACTGTCTGAGCAGGTGTCAGAGAGAGCTGCTCAGTCCCAGGTCAACCAGGAACCTG 294
Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
Db 295 AGGCGCTGTATGGACGAGACCATGAAGGAGTTGAAGGCTTACAAATCGGAACCTGAGGAA 354
Qy 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
Db 355 CAACGTGACCCCGGTGGCGGAGACGCGGCGACGGCTGTCCAAGGAGCTCGAGCGCGC 414
Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
Db 415 CAGGCCCGCTGGCGCGCGCATGGAGACGCTGTGGCGCGCTGTGGTGTGCTGCTGCCGCGC 474
Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
Db 475 GAGGTGCGGACCATGCTCGGCGCAGACCGAGGAGTGGCGGCTGCGCTCCCTCCAC 534
Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
Db 535 CTGGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGCCGATGCCGATGCCG 594
Qy 161 ValTyrGlnAlaGlyAlaArgGluGluValAlaGluArgGlyLeuSerAlaIleArgGluArg 180
Db 595 GTGTACCAAGCGCGGCGCGCGAGGCGCGGCGCGCTCAGCGCCATCCGCGAGCGC 654
Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
Db 655 CTGGGCGCCCTGTGGTGGAAACAGGCGCGCTCGGCGGAGAGTGGCGGCGGATGGAGAG 714
Qy 201 GlnProLeuGlnAlaGlnAlaThrGlyGluArgLeuArgAlaArgMetGluGlu 220
Db 715 CAGCCGCTACAGAGCGGCGCCAGGCTGTGGCGAGCGGCTGTGGCGCGGATGGAGAG 774
Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
Db 775 ATGGCAGCGCGGACCCGCGACCGCTTGGACGAGGTGAAGGAGCAGGTGGCGAGGTGGC 834
Qy 241 AlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
Db 835 GCCAAGCTGGAGGAGCAGGCGCCAGCATACGCTGCGAGGCGGAGGCTTCCAGGCGCGC 894
Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTyrAlaGlyLeuVal 280
Db 895 CTCGAAGCTGGTTCTGAGGCCCTGTGTGAAGACATGACGCGCCAGTGGCGCGGCTGGT 954
Qy 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
Db 955 GAGAGGTGCAGGCTGCCGTGGGCGACCGAGCGCGCCCTGTGCCCGGACCAATCAC 1011
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RESULT 13

US-10-852-335A-10
; Sequence 10, Application US/10852335A
; Publication No. US20050112129A1
; GENERAL INFORMATION:
; APPLICANT: HEIDI S. PHILLIPS
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumors of Gliial Origin
; FILE REFERENCE: P5103R1-US
; CURRENT APPLICATION NUMBER: US/10/852,335A
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 60/548,299
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/473,238
; PRIOR FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 190
; SEQ ID NO 10
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-852-335A-10

Alignment Scores:

Pred. No.: 9,78e-135 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-09-827-854A-2 (1-299) x US-10-852-335A-10 (1-1156)

QY	1	LyseValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp	20
DB	115	AAAGTGGAGCAAGCGGTGGAGACAGAGCCGAGCGCCGAGCTGCGCCAGACCGAGTGG	174
QY	21	GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal	40
DB	175	CAGAGCGCCAGCGCTGGAACTGGCACTGGGTGCTTTTGGGATTACCTGCGCTGGGTG	234
QY	41	GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu	60
DB	235	CAGACACTGTCTCAGCAGGTGCAGAGAGCTGCTCAGCTCCAGAGTCAACCCAGGAATG	294
QY	61	ArgAlaLeuMetAspGluThrMetLysGluLeuAlaTyrLysSerGluLeuGluGlu	80
DB	295	AGGCGCGTGTATGACGAGACCATGAGAGAGTTGAAGGCTTACAAATCGGAACTGGAGG	354
QY	81	GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaA	100
DB	355	CAACTGACCCCGTGGCGGAGGAGACGCGGCGCGCTGTCCAAGGAGCTGCAGGCGCG	414
QY	101	GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly	120
DB	415	CAGCGCGCGTGGCGCGGACATGGAGAGCTGTGCGCGCGCTGTGGTGCAGTACCGCGC	474
QY	121	GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValAlaArgLeuAlaSerHis	140
DB	475	GAGGTGAGGCGCATGCTCGGCGAGAGCAGGAGAGCTGGGGTGGCGCTCGCTCCAC	534
QY	141	LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla	160
DB	535	CTGGCAAGCTGCTTAAGCGGCTCTCCGCGATGCGCATGACCTGCAGAGAGCGCTGGCA	594
QY	161	ValTyrGlnAlaGlyAlaArgGluGlyAlaGluArgGlyLeuSerAlaIleArgGluArg	180
DB	595	GTGTACAGCGCGCGGCGCGGAGCGCGCGCGCTTCAGCGCCATCCCGAGCGC	654
QY	181	LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly	200
DB	655	CTGGGCGCGCTGTGGAGACAGGCGCGGTGGCGCGCGCTGTGGCTCTCCCTGGCGCG	714

QY	201	GlnProLeuGlnGluArgAlaGlnAlaTrpGlyGluArgLeuArgAlaArgMetGluGlu	220
DB	715	CAGCGCGCTACAGAGCGCGCCAGGCTTGGGCGAGCGGCTGCGCGCGGATGGAGGAG	774
QY	221	MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg	240
DB	775	ATGGGCGCGCGCGCGCGCGCGCTGGACAGAGGTGAAGAGAGAGGTGGCGGAGGTGGCG	834
QY	241	AlaLysLeuGluGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg	260
DB	835	GCCAGCTGGAGGAGCAGCGCCAGCAGATACGCTGCAGCGCGAGGCGCTTCCAGGCGCGC	894
QY	261	LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTrpAlaGlyLeuVal	280
DB	895	CTCAAGAGCGTGTTCAGGCGCGCTGGTGAAGACATGCAGCGCGAGTGGCGCGGTGGTG	954
QY	281	GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAenHis	299
DB	955	GAGAGGTGCAGGCTGCGGTGGGCGCCAGCGCGCGCTGTGCCAGCGCAATCAC	1011

RESULT 14

US-10-937-758A-106
; Sequence 106, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
; LENGTH: 1156
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(1014)
; OTHER INFORMATION:
US-10-937-758A-106

Alignment Scores:

Pred. No.: 9,78e-135 Length: 1156
Score: 1493.00 Matches: 299
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-09-827-854A-2 (1-299) x US-10-937-758A-106 (1-1156)

QY	1	LyseValGluGlnAlaValGluThrGluProGluProGluLeuArgGlnGlnThrGluTrp	20
DB	115	AAAGTGGAGCAAGCGGTGGAGACAGAGCCGAGCGCCGAGCTGCGCCAGACCGAGTGG	174
QY	21	GlnSerGlyGlnArgTrpGluLeuAlaLeuGlyArgPheTrpAspTyrLeuArgTrpVal	40
DB	175	CAGAGCGCGCGCGCTGGGAACTGGCACTGGGTGCTTTTGGGATTACCTGCGCTGGGTG	234
QY	41	GlnThrLeuSerGluGlnValGlnGluLeuLeuSerSerGlnValThrGlnGluLeu	60
DB	235	CAGACACTGTCTCAGCAGGTGCAGAGAGCTGCTCAGCTCCAGAGTCAACCCAGGAATG	294
QY	61	ArgAlaLeuMetAspGluThrMetLysGluLeuAlaTyrLysSerGluLeuGluGlu	80
DB	295	AGGCGCGTGTATGACGAGACCATGAGAGAGTTGAAGGCTTACAAATCGGAACTGGAGG	354
QY	81	GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaA	100
DB	355	CAACTGACCCCGTGGCGGAGGAGACGCGGCGCGCTGTCCAAGGAGCTGCAGGCGCG	414

Qy 101 GlnAlaArgLeuGluAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
 Db 415 CAGGCCCGCTGGCGCGGACATGAGAGAGCTGTGCGGCCCTGTGTGAGTACCGCGC 474
 Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
 Db 475 GAGGTGCAGGCCATGCTCGGCCAGACACGAGGAGCTGCGGTGCGCTGCGCTGCCAC 534
 Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuLeuLysArgLeuAla 160
 Db 535 CTGCGCAAGCTGCGTAAGCGCTCTCCGCGATCCGATGACCTGCAAGAGCGCTGCGCA 594
 Qy 161 ValTyrGlnAlaGlyAlaArgGluGluValAlaArgGlyLeuSerAlaIleArgGluArg 180
 Db 595 GTGTACAGCGCGGGGCCGAGGCGCGTGGCGGCGCGCTCAGCGCCATCCGCGAGCGC 654
 Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
 Db 655 CTGGGGCCCTGTGTGAACAGGCGCGTGGCGGAGCGCTGCGCGCGCTGCGCTGCCAC 714
 Qy 201 GlnProLeuGlnAlaArgAlaGlnAlaThrGlyGluArgLeuArgAlaArgMetGluGlu 220
 Db 715 CAGCCGCTACAGGAGCGGCGCCAGCGCTGGCGGAGCGCTGCGCGCGCTGCGCTGCCAG 774
 Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
 Db 775 ATGGCGAGCGGACCGCGCGCTGAGAGAGTGAAGGAGCGGTGGCGAGTGGCG 834
 Qy 241 AlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
 Db 835 GCCAAGCTGAGGAGCGGCGCCAGCAGATACGCTGCAGGCGGAGGCTTCCAGGCGCGC 894
 Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTyrAlaGlyLeuVal 280
 Db 895 CTCAAGAGCTGGTTCGAGCGCTTGGTGAAGACATGACGCGCCAGTGGCGCGGCTGGTG 954
 Qy 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
 Db 955 GAGNAGGTGAGGCTGCGTGGGCGACCGCGCGCCCTGTGCGCCAGCGCAATCAC 1011

RESULT 15

US-10-773-446-63
 ; Sequence 63, Application US/10773446
 ; Publication No. US20050176662A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INANA, GEORGE
 ; APPLICANT: MCLAREN, MARGARET
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING RETINAL
 ; TITLE OF INVENTION: DISEASES
 ; FILE REFERENCE: 39532-192229
 ; CURRENT APPLICATION NUMBER: US/10/773,446
 ; CURRENT FILING DATE: 2004-02-09
 ; NUMBER OF SEQ ID NOS: 131
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 63
 ; LENGTH: 1156
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-773-446-63

Alignment Scores:

Pred. No.:	9.78e-135	Length:	1156
Score:	1493.00	Matches:	299
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-09-827-854A-2 (1-299) x US-10-773-446-63 (1-1156)

Qy 1 LysValGluGlnAlaValGluThrGluProGluProGluArgGlnGlnThrGluTyr 20
 |||||

Db 115 AAGGTGAGCAAGCGTGGAGACAGAGCCGAGAGCCCGAGCTGCGCCAGCAGACCCAGTGG 174
 Qy 21 GlnSerGlyGlnArgTyrGluLeuAlaLeuGlyArgPheTyrAspTyrLeuArgTyrVal 40
 Db 175 CAGAGCGCGCAGCGCTGGGAACTGGCACTGGGTGCGCTTTTGGGATTACCTCGCTGGGTG 234
 Qy 41 GlnThrLeuSerGluGlnValGlnGluGluLeuSerSerGlnValThrGlnGluLeu 60
 Db 235 CAGACACTGCTGAGCAGAGTGCAGGAGAGCTGCTCAGCTCCAGGTCCACCCAGGAACCTG 294
 Qy 61 ArgAlaLeuMetAspGluThrMetLysGluLeuLysAlaTyrLysSerGluLeuGluGlu 80
 Db 295 AGGCGCTGATGGACGAGACCATGAGGAGTGAAGGCCTACAAATCGGAATCGAGGAA 354
 Qy 81 GlnLeuThrProValAlaGluGluThrArgAlaArgLeuSerLysGluLeuGlnAlaAla 100
 Db 355 CAATGACCCCGTGGCGGAGGACCGCGGCTGTCCAAAGGAGCTGACGCGCGC 414
 Qy 101 GlnAlaArgLeuGlyAlaAspMetGluAspValCysGlyArgLeuValGlnTyrArgGly 120
 Db 415 CAGGCCCGCTGGCGCGGACATGAGAGAGCTGTGCGCGCCCTGTGTGAGTACCGCGC 474
 Qy 121 GluValGlnAlaMetLeuGlyGlnSerThrGluGluLeuArgValArgLeuAlaSerHis 140
 Db 475 GAGGTGCAGGCCATGCTCGGCCAGACACGAGGAGCTGCGGTGCGCTGCGCTGCCAC 534
 Qy 141 LeuArgLysLeuArgLysArgLeuLeuArgAspAlaAspLeuGlnLysArgLeuAla 160
 Db 535 CTGCGCAAGCTGCGTAAGCGCTCTCCGCGATCCGATGACCTGCAAGAGCGCTGCGCA 594
 Qy 161 ValTyrGlnAlaGlyAlaArgGluGluValAlaArgGlyLeuSerAlaIleArgGluArg 180
 Db 595 GTGTACAGCGCGGGGCCGAGGCGCGTGGCGGCGCGCTCAGCGCCATCCGCGAGCGC 654
 Qy 181 LeuGlyProLeuValGluGlnGlyArgValArgAlaAlaThrValGlySerLeuAlaGly 200
 Db 655 CTGGGGCCCTGTGTGAACAGGCGCGTGGCGGCGCGCTGCGCGCGCTGCGCTGCCAC 714
 Qy 201 GlnProLeuGlnAlaArgAlaGlnAlaThrGlyGluArgLeuArgAlaArgMetGluGlu 220
 Db 715 CAGCCGCTACAGGAGCGGCGCCAGCGCTGGGCGAGCGGCTGCGCGCGCTGCGCTGCCAG 774
 Qy 221 MetGlySerArgThrArgAspArgLeuAspGluValLysGluGlnValAlaGluValArg 240
 Db 775 ATGGCGAGCGGACCGCGCGCTGAGAGAGTGAAGGAGCGGTGGCGAGTGGCG 834
 Qy 241 AlaLysLeuGluGlnAlaGlnGlnIleArgLeuGlnAlaGluAlaPheGlnAlaArg 260
 Db 835 GCCAAGCTGAGGAGCGGCGCCAGCAGATACGCTGCAGGCGGAGGCTTCCAGGCGCGC 894
 Qy 261 LeuLysSerTrpPheGluProLeuValGluAspMetGlnArgGlnTyrAlaGlyLeuVal 280
 Db 895 CTCAAGAGCTGGTTCGAGCGCTTGGTGAAGACATGACGCGCCAGTGGCGCGGCTGGTG 954
 Qy 281 GluLysValGlnAlaAlaValGlyThrSerAlaAlaProValProSerAspAsnHis 299
 Db 955 GAGNAGGTGAGGCTGCGTGGGCGACCGCGCGCCCTGTGCGCCAGCGCAATCAC 1011

Search completed: June 15, 2006, 00:44:28
 Job time : 2165.08 secs

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 19:02:13 ; Search time 557.375 Seconds

(without alignments)
3097.698 Million cell updates/sec

Title: US-09-827-854A-13

Perfect score: 92

Sequence: 1 MKVLWAALLVFLAGCQA 18

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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- 4: gb_pl.*
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- 8: gb_sy.*
- 9: gb_un.*
- 10: gb_vi.*
- 11: gb_ov.*
- 12: gb_htg.*
- 13: gb_in.*
- 14: gb_om.*
- 15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	71	2	I15467 Sequence 10
2	92	100.0	71	2	I69313 Sequence 10
3	92	100.0	93	2	AR211787 Sequence

4	92	100.0	117	8	ASTOOL10
5	92	100.0	275	5	HSJ2127
6	92	100.0	405	2	BD025884
7	92	100.0	405	2	AR726145
8	92	100.0	405	2	AX886274
9	92	100.0	478	2	AX330507
10	92	100.0	478	2	AX335168
11	92	100.0	478	2	AX409845
12	92	100.0	499	2	AX427528
13	92	100.0	583	2	AR578700
14	92	100.0	660	2	A62340
15	92	100.0	660	2	A62342
16	92	100.0	660	2	A62344
17	92	100.0	660	2	AR075563
18	92	100.0	1107	2	BD084811
19	92	100.0	1110	2	E00359
20	92	100.0	1110	2	E00823
21	92	100.0	1110	2	E08423
22	92	100.0	1147	2	AX302545
23	92	100.0	1156	2	BD004277
24	92	100.0	1156	2	BD004278
25	92	100.0	1156	2	BD004279
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27	92	100.0	1156	2	CQ785970
28	92	100.0	1156	2	CQ875269
29	92	100.0	1156	2	CQ896276
30	92	100.0	1156	2	CQ963896
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35	92	100.0	1156	5	HUMAPOE3
36	92	100.0	1157	2	DD166085
37	92	100.0	1157	2	I15975
38	92	100.0	1157	2	AX333278
39	92	100.0	1157	2	AX409597
40	92	100.0	1157	5	HUMAPOE
41	92	100.0	1178	5	MEAPOE
42	92	100.0	1186	5	BC003557
43	92	100.0	1291	2	AR531680
44	92	100.0	1550	5	BC072022
45	92	100.0	1779	5	AK130027

ALIGNMENTS

RESULT 1

I15467

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Location/Qualifiers

1..71

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/mol_type="unassigned DNA"

ORIGIN

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Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

2.11e-09

92.00

100.0%

100.0%

100.0%

Length:

Matches:

Conservative:

Mismatches:

Indels:

71

18

0

0

0

linear

PAT 02-APR-1996

71 bp

DNA

Sequence 10 from patent US 5466593.

I15467

I15467.1

GI:1250375

Unknown.

Unclassified.

1 (bases 1 to 71)

Shimomura,T., Yamada,K., Morimoto,Y., Kitamura,N. and Miyazawa,K.

Hepatocyte growth factor activating protease and gene encoding the

protease

Patent: US 5466593-A 10 14-NOV-1995;

FEATURES
source

Location/Qualifiers
1..275
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/clone="ICRFp507d2127"
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/standard_name="apolipoprotein E"
/note="homologous to K00396"
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38..>275
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/db_xref="GI:1263123"
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/db_xref="InterPro:IPR000074"
/db_xref="UniProtKB/TrEMBL:Q6LA97"
/translation="MKVLWALLVTFLAGCOAKVEQAVETPEPELQQTEWQSGQRW
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Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-09-827-854a-13 (1-18) x HSJ2127 (1-275)

Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 38 ATGAAGGTTCTGTGGCTGCTGTGTCACATTCTGGCAGGATGCCAGGCC 91

RESULT 6

BD025884
LOCUS
DEFINITION
Sequence tag and encoded human protein.
ACCESSION
BD025884
VERSION
BD025884.1 GI:22567107
KEYWORDS
JP 2001269182-A/2130
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 405)
AUTHORS
Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE
Sequence tag and encoded human protein
JOURNAL
Patent: JP 2001269182-A 2130 02-OCT-2001;
GENSET

COMMENT

OS Homo sapiens (human)
PN JP 2001269182-A/2130
PD 02-OCT-2001
PR 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
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CC
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
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FEATURES
source

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Pred. No.: 1.22e-08 Length: 405
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0
US-09-827-854a-13 (1-18) x BD025884 (1-405)
Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 75 ATGAAGGTTCTGTGGCTGCTGTGTCACATTCTGGCAGGATGCCAGGCC 128
RESULT 7
LOCUS
DEFINITION
Sequence 2137 from patent US 6783961.
ACCESSION
AR726145
VERSION
AR726145.1 GI:77419885
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 405)
AUTHORS
Edwards, J.-B.D.M., Duclert, A. and Giordano, J.-Y.
TITLE
Expressed sequence tags and encoded human proteins
JOURNAL
Patent: US 6783961-A 2137 31-AUG-2004;
Genset S.A.;
FRX;
FEATURES
source
1..405
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.22e-08 Length: 405
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0
US-09-827-854a-13 (1-18) x AR726145 (1-405)
Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 75 ATGAAGGTTCTGTGGCTGCTGTGTCACATTCTGGCAGGATGCCAGGCC 128
RESULT 8
LOCUS
DEFINITION
Sequence 2137 from Patent EP1033401.
ACCESSION
AX886274
VERSION
AX886274.1 GI:40043271
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE
Expressed sequence tags and encoded human proteins
JOURNAL
Patent: EP 1033401-A 2137 06-SEP-2000;
Genset (FR)
FEATURES
source
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Location/Qualifiers

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119..>403
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/protein_id="CAP00412.1"
/db_xref="GI:40043272"
/translation="MPQGAGSGDRAGAAPZTEWQSGORWELALGRFWDVLRWVQ
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ORIGIN
Alignment Scores:
Pred. No.: 1.22e-08 Length: 405
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-827-854A-13 (1-18) x AX886274 (1-405)

Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 75 ATGAAGGTTCTGTGGGCTGGCTGTGTGCACATTCTTGGCAGGATGCCAGGCC 128

RESULT 9
LOCUS AX330507/c 478 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 1016 from Patent WO0194629.
ACCESSION AX330507
VERSION AX330507.1 GI:18103485
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 1016 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source
Location/Qualifiers
1..478
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ORIGIN
Alignment Scores:
Pred. No.: 1.44e-08 Length: 478
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-827-854A-13 (1-18) x AX330507 (1-478)

Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 396 ATGAAGGTTCTGTGGGCTGGCTGTGTGCACATTCTTGGCAGGATGCCAGGCC 343

RESULT 10
AX335168/c
LOCUS AX335168 478 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 5677 from Patent WO0194629.
ACCESSION AX335168
VERSION AX335168.1 GI:18125887
KEYWORDS

```

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 5677 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Alignment Scores:
Pred. No.: 1.44e-08 Length: 478
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-827-854A-13 (1-18) x AX335168 (1-478)

Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 396 ATGAAGGTTCTGTGGGCTGGCTGTGTGCACATTCTTGGCAGGATGCCAGGCC 343

RESULT 11
AX409845/c
LOCUS AX409845 478 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 2492 from Patent WO0229103.
ACCESSION AX409845
VERSION AX409845.1 GI:21442550
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 2492 11-APR-2002;
GENE LOGIC INC (US)
FEATURES
source
Location/Qualifiers
1..478
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="EMBL/GenBank Accession No. N33009"

ORIGIN
Alignment Scores:
Pred. No.: 1.44e-08 Length: 478
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-827-854A-13 (1-18) x AX409845 (1-478)

Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 396 ATGAAGGTTCTGTGGGCTGGCTGTGTGCACATTCTTGGCAGGATGCCAGGCC 343

RESULT 12

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AX427528      AX427528      499 bp      DNA      linear      PAT 20-JUN-2002
LOCUS          Sequence 38 from Patent WO0121836.
ACCESSION      AX427528
VERSION        AX427528.1  GI:21537674
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE      1
AUTHORS        Hodgson,D.M., Lincoln,S.E., Russo,F.D., Spiro,P.A., Banville,S.C.,
               Bratcher, Shawn,R., Dufour,G.F., Cohen,H.J., Rosen,B.H., Shah,P.,
               Chalup,M.S., Hillman,J.L., Jones,A.L., Yu,J.Y., Greenawalt,L.B.,
               Panzer,S.R., Roseberry,A.M., Wright,R.J., Chen,W., Liu,T.,
               Yap,P.E., Stockreiter,T.K., Amshey,S. and Fong,W.T.
TITLE          Molecules for diagnostics and therapeutics
JOURNAL        Patent: WO 0121836-A 38 29-MAR-2001;
               Incyte Genomics, Inc. (US)
FEATURES       Location/Qualifiers
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Score:          92.00      Matches:      18
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Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    100.0%      Indels:      0
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Qy      1 MetLysValLeuTTPAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db      128 ATGAAGGTTCTGTGGGCTGCGTGTCTGTCACATTCCTGGCAGGATGCCAGGCC 181

RESULT 13
AR578700      AR578700      583 bp      DNA      linear      PAT 14-DEC-2004
LOCUS          Sequence 876 from patent US 6783969.
ACCESSION      AR578700
VERSION        AR578700.1  GI:56581496
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 583)
AUTHORS        Tang,Y.T., Goodrich,R.W., Asundi,V. and Drmanac,R.T.
TITLE          Cathepsin V-like polypeptides
JOURNAL        Patent: US 6783969-A 876 31-AUG-2004;
               Nuvelo, Inc.; Sunnyvale, CA
FEATURES       Location/Qualifiers
source         1..583
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Pred. No.:      1.76e-08      Length:      583
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Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    100.0%      Indels:      0
DB:             2          Gaps:      0

US-09-827-854A-13 (1-18) x AR578700 (1-583)
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Qy      1 MetLysValLeuTTPAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db      56 ATGAAGGTTCTGTGGGCTGCGTGTCTGTCACATTCCTGGCAGGATGCCAGGCC 109

RESULT 14
A62340        A62340        660 bp      DNA      linear      PAT 09-MAR-1998
LOCUS          Sequence 28 from Patent WO9712992.
ACCESSION      A62340
VERSION        A62340.1    GI:3716293
KEYWORDS       unidentified
SOURCE         unidentified
ORGANISM       unclassified sequences.
REFERENCE      1
AUTHORS        Van,L.F., Burbach,J.P. and Grosveld,F.G.
TITLE          DIAGNOSIS METHOD AND REAGENTS
JOURNAL        Patent: WO 9712992-A 28 10-APR-1997;
               ROYAL NETHERLANDS ACADEMY OF A (NL)
               Other publication AU 7142796 970428.
FEATURES       Location/Qualifiers
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               /db_xref="GI:3716294"
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               ETRPELROQTWOSQORWELALGREFWDLRWVQTLSEQVQBELLSQVTELRALM
               DETMKELKAYKSELEQLTPVASETRALSKELOTAQARLGADMEDVCGRLAVQYRGEV
               QAMLCQSTELRVLRLASHLRKLRLLRDPDDLQRLAVYQAGAREGLSIRER
               LG"
ORIGIN
Alignment Scores:
Pred. No.:      1.99e-08      Length:      660
Score:          92.00      Matches:      18
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    100.0%      Indels:      0
DB:             2          Gaps:      0

US-09-827-854A-13 (1-18) x A62340 (1-660)
Qy      1 MetLysValLeuTTPAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db      62 ATGAAGGTTCTGTGGGCTGCGTGTCTGTCACATTCCTGGCAGGATGCCAGGCC 115

RESULT 15
A62342        A62342        660 bp      DNA      linear      PAT 09-MAR-1998
LOCUS          Sequence 30 from Patent WO9712992.
ACCESSION      A62342
VERSION        A62342.1    GI:3716295
KEYWORDS       unidentified
SOURCE         unidentified
ORGANISM       unclassified sequences.
REFERENCE      1
AUTHORS        Van,L.F., Burbach,J.P. and Grosveld,F.G.
TITLE          DIAGNOSIS METHOD AND REAGENTS
JOURNAL        Patent: WO 9712992-A 30 10-APR-1997;
               ROYAL NETHERLANDS ACADEMY OF A (NL)
               Other publication AU 7142796 970428.
FEATURES       Location/Qualifiers
source         1..660
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
ORIGIN
```

Alignment Scores:
 Pred. No.: 1.99e-08 Length: 660
 Score: 92.00 Matches: 18
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-09-827-854A-13 (1-18) x A62342 (1-660)

Qy 1 MetLysValLeuTrpAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
 Db 62 ATGAAGGTTCTGTGGGCTGGGTTGCTGTGTCACATTCTGGCAGGATGCCAGGCC 115

Search completed: June 14, 2006, 21:46:04
 Job time : 560.375 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model
Run on: June 14, 2006, 18:51:12 ; Search time 61.9495 Seconds
(without alignments)
3038.776 Million cell updates/sec

Title: US-09-827-854A-13
Perfect score: 92
Sequence: 1 MKVLWAAALLVTFLLAGCOA 18

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 524920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-DB=N Geneseq -QFMT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPFCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs04
-USER=US09827854 @CGI_1_942 @runat_14062006.081823_26716 -NCPUs=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8.*
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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
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7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	79	10 ADE15845	Ade15845 Primer #1
2	92	100.0	93	2 AAV08172	Aav08172 Primer fo
3	92	100.0	93	6 ABL57678	Abi57678 Human mat

4	92	100.0	333	10	ACD95309	Human col
5	92	100.0	405	3	AAC02139	Human sec
6	92	100.0	407	6	ABK34238	Human CDN
7	92	100.0	440	14	ADV76096	Human col
8	92	100.0	441	14	ADV76095	Human col
9	92	100.0	445	9	ACH21663	Human adu
c 10	92	100.0	478	6	ABL67340	Thyroid c
c 11	92	100.0	478	6	ABL62679	Colon ade
c 12	92	100.0	478	6	ABN95994	Gene #249
13	92	100.0	480	10	ADJ57602	Human apo
14	92	100.0	499	4	AAS03049	Human dia
15	92	100.0	583	6	ABZ11994	Human pol
16	92	100.0	583	12	ADM44512	Novel hum
17	92	100.0	660	2	AAT69792	Partial h
18	92	100.0	684	12	ADG71903	Human CDN
19	92	100.0	684	12	ADJ87240	Human G p
20	92	100.0	709	12	ADG71915	Human CDN
21	92	100.0	709	12	ADJ87252	Human G p
22	92	100.0	718	12	ADG71909	Human CDN
23	92	100.0	718	12	ADJ87246	Human G p
24	92	100.0	788	12	ADG71907	Human CDN
25	92	100.0	788	12	ADJ87244	Human G p
26	92	100.0	802	12	ADG71905	Human CDN
27	92	100.0	802	12	ADJ87242	Human G p
28	92	100.0	954	6	AAD26035	Human apo
29	92	100.0	954	14	ADV42852	Human psy
30	92	100.0	1107	2	AAX75756	Human apo
31	92	100.0	1110	1	AAN50450	Sequence
32	92	100.0	1110	1	AAN60409	Human apo
33	92	100.0	1147	5	ABA83113	Apolipopr
34	92	100.0	1154	13	ADQ86961	Human tum
35	92	100.0	1156	4	AAF84315	Human Apo
36	92	100.0	1156	4	AAF84314	Human Apo
37	92	100.0	1156	4	AAF84316	Human Apo
38	92	100.0	1156	6	ABT13008	Human apo
39	92	100.0	1156	6	AAD22052	Human apo
40	92	100.0	1156	6	AAD22047	Human apo
41	92	100.0	1156	6	AAD22048	Human apo
42	92	100.0	1156	6	AAD22051	Human apo
43	92	100.0	1156	6	AAD22049	Human apo
44	92	100.0	1156	6	AAD22050	Human apo
45	92	100.0	1156	8	ACA64743	Apolipopr

ALIGNMENTS

RESULT 1
ADE15845
ID ADE15845 standard; DNA; 79 BP.
XX
AC ADE15845;
XX
DT 29-JAN-2004 (first entry)
XX
DE Primer #12 of the invention.
XX
KW nicotinic acetylcholine receptor; AChR; Neuroprotective;
KW myasthenia gravis; ss; primer.
XX
OS Synthetic.
XX
PN WO2003087373-A2.
XX
PD 23-OCT-2003.
XX
PF 15-APR-2003; 2003WO-GR000014.
XX
PR 17-APR-2002; 2002GR-00100190.
XX
PA (HELL-) HELLENIC PASTEUR INST.
PA (ASFR-) ASSOC FR CONTRE MYOPATHIES.
PA (TZAR/) TZARTOS S.
PA (MAMA/) MAMALAKI A.

CC inflammatory, and anti-arthritis activity. The polynucleotide may have a
CC use in gene therapy. The MMP-ABT polynucleotides and proteins are useful
CC for detecting, diagnosing, staging, monitoring, prognosing, preventing or
CC treating cancer or inflammatory diseases (e.g. arthritis). The MMP-ABT
CC proteins and polynucleotides are also useful developing therapeutic
CC agents that affect MMP function

XX Sequence 93 BP; 22 A; 21 C; 27 G; 23 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.1e-07 Length: 93
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x ABL57678 (1-93)

Qy 1 MetLysValLeuTPAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 16 ATGAAGGTTCTGTGGCTGCTTCTGTGTACATCTCTGGCAGGATGCCAGGCC 69

RESULT 4

ACD95309
ID ACD95309 standard; cDNA; 333 BP.

AC ACD95309;

XX 23-SEP-2003 (first entry)

DE Human colon cancer cell expressed cDNA #3721.

KW Open reading frame detection; genome sequencing; colon cancer;
KW breast cancer; population genome analysis; genetic shift; cancer;
KW antibiotic resistance; antibiotic non-tolerance; congenital disease;
KW agriculture; food crop genome; resistance gene; retrovirus;
KW influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KW gene; ss.

XX Homo sapiens.

XX US2002155438-A1.

XX 24-OCT-2002.

XX 27-SEP-1999; 99US-00406117.

XX 20-NOV-1998; 98US-00196716.

XX (SIMP/) SIMPSON A J G.

PA (NETO/) NETO E D.

PA (BREN/) BRENTANI R R.

XX Simpson AJG, Neto ED, Brentani RR;

DR WPI; 2003-182626/18.

XX Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.

XX Example 9; Page 543; 959pp; English.

XX The invention describes a method of determining open reading frames in
CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (I), amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing resulting
CC nucleic acids. The method is useful for: determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a

CC nucleotide sequence of an open reading frame; for preparing a contig,
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library

XX Sequence 333 BP; 73 A; 83 C; 120 G; 55 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 2.26e-06 Length: 333
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-09-827-854A-13 (1-18) x ACD95309 (1-333)

Qy 1 MetLysValLeuTPAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 54 ATGAAGGTTCTGTGGCTGCTTCTGTGTACATCTCTGGCAGGATGCCAGGCC 107

RESULT 5

ACD02139

ID AAC02139 standard; cDNA; 405 BP.

XX AAC02139;

XX 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 2137.

XX Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

DR P-PSDB; AAG02133.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 2137; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors
XX
SQ Sequence 405 BP; 90 A; 105 C; 149 G; 60 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.85e-06 Length: 405
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservatively: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-13 (1-18) x AAC02139 (1-405)
Qy 1 MetLysValLeuTrpAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 75 ATGAAGGTTCTGTGGGCTGCGTGTGCTGCACATTCTGGCAGATGCCAGGCC 128

RESULT 6
ABK34238
ID ABK34238 standard; cDNA; 407 BP.
AC ABK34238;
XX
XX 08-MAY-2002 (first entry)
XX
XX Human cDNA for novel secreted protein, SEQ ID 7.
XX
XX Human; ss, gene; secreted protein; immune deficiency; viral infection;
XX bacterial infection; fungal infection; autoimmune disorder; burn;
XX rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;
XX diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;
XX Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;
XX coagulation disorder; haemophilia; inflammatory disorder; ulcer;
XX tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;
XX lymphoid cell deficiency.
XX
XX Homo sapiens.
XX
XX WO200177290-A2.
XX
XX 18-OCT-2001.
XX
XX 29-MAR-2001; 2001WO-US010295.
XX
XX 06-APR-2000; 2000US-0194941P.
XX
XX (GEM) GENETICS INST INC.
XX
XX Wong GG, Clark HF, Fecthel K, Agostino MJ, Howes SH, Resnick RJ;
XX Gulukota K, Graham JR;
XX WPI; 2002-179323/23.
XX
XX Six hundred and twenty five polynucleotides derived from a variety of

PT human tissue sources which encode secreted proteins, useful for treating
PT immune deficiencies and disorders such as autoimmune disorders.
XX
PS Claim 1; Page 70; 339pp; English.
XX
CC The invention relates to 625 polynucleotides which have been derived from
CC a variety of human tissue sources and which encode novel secreted
CC proteins, their complements and sequences that hybridise to them. Also
CC included are a vector comprising the polynucleotide, a host cell
CC transformed with the vector, the proteins encoded by the polynucleotides,
CC antibodies that bind to the proteins and identification of modulators of
CC the proteins or the expression of the polynucleotide. The polynucleotides
CC can be used as probes for the identification and isolation of full length
CC cDNA and genomic DNA. The polynucleotides and proteins can also be used
CC as nutritional supplements. The protein is useful in the treatment of
CC various immune deficiencies and disorders such as viral infections,
CC bacterial infections, fungal infections, autoimmune disorders (e.g.
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and
CC diabetes) and allergic reactions and conditions (e.g. asthma). They are
CC also useful for treating neurodegenerative diseases (e.g. Alzheimer's
CC disease, Parkinson's disease), liver fibrosis, coagulation disorders
CC (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and
CC tumours. They are also useful for tissue regeneration, for wound healing
CC and in the treatment of burns, incisions and ulcers. The proteins are
CC also useful for regulating haematopoiesis, for treating myeloid or
CC lymphoid cell deficiencies. The present sequence is one of the 625 cDNA
CC sequences encoding a secreted protein
XX
SQ Sequence 407 BP; 88 A; 103 C; 158 G; 58 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.86e-06 Length: 407
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservatively: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x ABK34238 (1-407)
Qy 1 MetLysValLeuTrpAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 20 ATGAAGGTTCTGTGGGCTGCGTGTGCTGCACATTCTGGCAGATGCCAGGCC 73

RESULT 7
ADV76096
ID ADV76096 standard; DNA; 440 BP.
XX
XX ADV76096;
XX
XX 10-MAR-2005 (first entry)
XX
XX Human colon tumor cell downregulated gene SEQ ID NO 2937.
XX
XX ds, gene; cancer; neoplasm; cytostatic.
XX
XX Homo sapiens.
XX
XX WO2004110345-A2.
XX
XX 23-DEC-2004.
XX
XX 28-OCT-2003; 2003WO-US034019.
XX
XX 29-OCT-2002; 2002US-0422176P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Bourner MJ, Bu JJ, Head RD, Hippenmeyer PJ, Klein BK;
XX Mazzarella RA, Staten NR;
XX WPI; 2005-039958/04.
XX
XX

PT New antibody that immunospecifically binds to p-cadherin, useful in
PT preparing a composition for treating or preventing a cancer-associated
PT disorder.
XX
XX Disclosure; SEQ ID NO 2937; 257pp; English.
XX
CC The invention relates to an antibody immunospecifically binds to p-
CC cadherin or its fragment. The antibody is useful in preparing a
CC composition for treating or preventing a cancer-associated disorder. The
CC present sequence represents a gene downregulated in human colon cancer
CC cells.
XX
XX Sequence 440 BP; 94 A; 114 C; 168 G; 62 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 3.13e-06 Length: 440
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservativity: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0

US-09-827-854A-13 (1-18) x ADV76096 (1-440)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
|||||
Db 57 ATGAAGGTTCTGTGGCTGCTTCTGTCACATTCCTGGCAGGATGCCAGGCC 110
|||||

RESULT 8
ADV76095
ID ADV76095 standard; DNA; 441 BP.
XX
AC ADV76095;
XX
XX 10-MAR-2005 (first entry)
XX
XX Human colon tumor cell downregulated gene SEQ ID NO 2936.
XX
XX ds; gene; cancer; neoplasm; cytostatic.
XX
XX Homo sapiens.
XX
XX WO2004110345-A2.
XX
XX 23-DEC-2004.
XX
XX 28-OCT-2003; 2003WO-US034019.
XX
XX 29-OCT-2002; 2002US-0422176P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Bourner MJ, Bu JJ, Head RD, Hippenmeyer PJ, Klein BK;
XX Mazzarella RA, Staten NR;
XX
XX WPI; 2005-039958/04.
XX
XX New antibody that immunospecifically binds to p-cadherin, useful in
XX preparing a composition for treating or preventing a cancer-associated
XX disorder.
XX
XX Disclosure; SEQ ID NO 2936; 257pp; English.
XX
CC The invention relates to an antibody immunospecifically binds to p-
CC cadherin or its fragment. The antibody is useful in preparing a
CC composition for treating or preventing a cancer-associated disorder. The
CC present sequence represents a gene downregulated in human colon cancer
CC cells.
XX
XX Sequence 441 BP; 98 A; 115 C; 166 G; 62 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.14e-06 Length: 441

Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservativity: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0
US-09-827-854A-13 (1-18) x ADV76095 (1-441)
Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
|||||
Db 56 ATGAAGGTTCTGTGGCTGCTTCTGTCACATTCCTGGCAGGATGCCAGGCC 109
|||||

RESULT 9

ACH21663
ID ACH21663 standard; cDNA; 445 BP.

XX
AC ACH21663;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human adult ovary cDNA #43.
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
XX
XX US2003073623-A1.
XX
XX 17-APR-2003.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRMA/) DRMANAC R T.
XX (LABA/) LABAT I.
XX (STAC/) STACHE-CRAIN B.
XX (DICK/) DICKSON M C.
XX (JONE/) JONES L W.

Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 8875; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversities, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030073623

XX Sequence 445 BP; 98 A; 113 C; 161 G; 72 T; 0 U; 1 Other;

Alignment Scores:

```
Pred. No.: 3.18e-06 Length: 445
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-09-827-854A-13 (1-18) x ACH21663 (1-445)
Qy 1 MetLysValLeuTrpAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 169 ATGAAGGTTCTGTGGGCTGGTGTGCACATTCTGGCAGGATGCCAGGCC 222

RESULT 10
ABL67340/c
ID ABL67340 standard; DNA; 478 BP.
XX
AC ABL67340;
XX
DT 15-MAY-2002 (first entry)
XX
DE Thyroid cancer related gene sequence SEQ ID NO:5677.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 08-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0231313P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
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PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
XX Claim 1; SEQ ID NO 5677; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 847 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
XX Sequence 478 BP; 72 A; 180 C; 123 G; 101 T; 0 U; 2 Other;
SQ
Alignment Scores:
Pred. No.: 3.45e-06 Length: 478
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x ABL67340 (1-478)
Qy 1 MetLysValLeuTrpAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 396 ATGAAGGTTCTGTGGGCTGGTGTGCACATTCTGGCAGGATGCCAGGCC 343

RESULT 11
ABL62679/c
ID ABL62679 standard; DNA; 478 BP.
XX
AC ABL62679;
XX
DT 15-MAY-2002 (first entry)
XX
DE Colon adenocarcinoma related gene sequence SEQ ID NO:1016.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
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Alignment Scores: 3.45e-06 Length: 478
 Pred. No.: 92.00 Matches: 18
 Score: 100.0% Conservatives: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x ABN95994 (1-478)
 QY 1 MetLysValLeuTrpAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
 Db 396 ATGAAGGTTCTGTGGCTGCTGTGGTACATTCTGCAGGATGCCAGGCC 343

RESULT 13
 ADJ57602
 ID ADJ57602 standard; DNA; 480 BP.
 XX AC ADJ57602;
 XX DT 06-MAY-2004 (first entry)
 XX DE Human apolipoprotein E DNA sequence.
 XX KW SNP; single nucleotide polymorphism; gene expression; genotyping;
 XX KW apolipoprotein E; apoB; human; gene; ds.
 XX OS Homo sapiens.
 XX PN WO2003065146-A2.
 XX PD 07-AUG-2003.
 XX PF 02-JAN-2003; 2003WO-US000128.

25-JAN-2002; 2002US-0352039P.
 28-JAN-2002; 2002US-0352356P.
 01-APR-2002; 2002US-0369127P.
 03-APR-2002; 2002US-036957P.
 09-APR-2002; 2002US-0370921P.
 26-APR-2002; 2002US-0376171P.
 06-MAY-2002; 2002US-0380057P.
 28-MAY-2002; 2002US-0383627P.
 29-MAY-2002; 2002US-0383954P.
 21-JUN-2002; 2002US-0390708P.
 05-JUL-2002; 2002US-0394115P.
 31-JUL-2002; 2002US-0399860P.
 (APPL-) APPLERA CORP.
 Koehler RT, Livak KJ, Stevens J, De La Vega FM, Rhodes M;
 Bellon LR, Dailey D, Ziegler J, Williams J, Madden D, Gilbert DA;
 Scafe CR, Avi-Itzhak HI, Webster MN, Wang YN, Spier EG, You X;
 Hemken H, Titus A, Xu L, Curlee J, Heil J, Glanowski S, Scott J;
 Winn-Deen E, McCullen I, Wu L, Gire C, Sprague A, Eddins S;
 WPI; 2003-679499/64.
 GENBANK; M10065.

Providing to consumer, assays for presence/expression of genetic material, by providing web-based user interface to receive order for stock assays, request for design and order for custom assays, and delivering assay.
 Disclosure; Fig 9; 332pp; English.
 The invention provides methods and assays for ordering assays which detect single nucleotide polymorphisms (SNPs) or gene expression. It provides to a consumer, assays to detect presence or expression of genetic material, by providing a web-based user interface to receive an order for one or more stock assays, providing a web-based user interface to receive a request for design of one or more custom assays and an order

CC for the custom assays, and delivering to the consumer at least one custom or stock assay in response to the order. The methods use PCR and RT-PCR CC procedures. The present sequence represents a human apolipoprotein E CC (apoE) DNA sequence.

SQ Sequence 480 BP; 99 A; 137 C; 178 G; 66 T; 0 U; 0 Other;

Alignment Scores: 3.47e-06 Length: 480
 Pred. No.: 92.00 Matches: 18
 Score: 100.0% Conservatives: 0
 Percent Similarity: 100.0% Mismatches: 0
 Best Local Similarity: 100.0% Indels: 0
 Query Match: 100.0% Gaps: 0
 DB: 10

US-09-827-854A-13 (1-18) x ADJ57602 (1-480)

QY 1 MetLysValLeuTrpAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
 Db 61 ATGAAGGTTCTGTGGCTGCTGTGGTACATTCTGCAGGATGCCAGGCC 114

RESULT 14
 AAS03049
 ID AAS03049 standard; cDNA; 499 BP.
 XX AC AAS03049;
 XX DT 29-AUG-2001 (first entry)
 XX DE Human diagnostic and therapeutic (dithp) cDNA sequence #38.
 XX KW Human diagnostic and therapeutic molecule; dithp; gene therapy;
 KW thalassemia; cardiovascular disorder; cell proliferative disorder;
 KW cancer; neurodegenerative disorder; autoimmune disorder;
 KW infectious disorder; inflammatory disorder; developmental disorder;
 KW Incyte ID number 3465999dec; secreted and extracellular molecule; ss.

Homo sapiens.
 WO200121836-A2.
 29-MAR-2001.
 19-SEP-2000; 2000WO-US025643.
 23-SEP-1999; 99US-0155760P.
 24-SEP-1999; 99US-0155939P.
 24-SEP-1999; 99US-0156294P.
 28-SEP-1999; 99US-0156565P.
 28-SEP-1999; 99US-0156624P.
 28-SEP-1999; 99US-0156625P.
 24-NOV-1999; 99US-0167410P.
 24-NOV-1999; 99US-0167517P.
 24-NOV-1999; 99US-0167520P.
 24-NOV-1999; 99US-0167521P.
 24-NOV-1999; 99US-0167522P.
 24-NOV-1999; 99US-0167542P.
 24-NOV-1999; 99US-0167543P.
 29-NOV-1999; 99US-0167943P.
 29-NOV-1999; 99US-0167945P.
 30-NOV-1999; 99US-0168197P.
 30-NOV-1999; 99US-0168265P.
 30-NOV-1999; 99US-0168429P.
 30-NOV-1999; 99US-0168432P.
 01-DEC-1999; 99US-0168468P.
 01-DEC-1999; 99US-0168599P.
 02-DEC-1999; 99US-0168611P.
 02-DEC-1999; 99US-0168613P.
 02-DEC-1999; 99US-0168857P.
 (INCY-) INCYTE GENOMICS INC.
 PA Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;
 XX

PI Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;
PI Hillman JL, Jones AL, Yu JY, Greenawalt LB, Panzer SR, Roseberry AM,
PI Wright RJ, Chen W, Liu TP, Yap PE, Stockdreher TK, Amshey S;
PI Fong WT;

XX WPI; 2001-281607/29.

XX Novel diagnostic and therapeutic polynucleotides, used in disease
XX diagnosis and for gene therapy of conditions such as cancer and
XX thalassemia.

XX Claim 1; Page 274; 299pp; English.

XX The present sequence for human diagnostic and therapeutic (dithp) cDNA
XX sequence #38 is 1 of 71 (AAS03012-AAS03082) novel sequences described in
XX the invention. The present sequence (Incye ID No: 3465999dec) encodes a
XX secreted and extracellular molecule. The dithp polynucleotides may be
XX used to diagnose a condition or disorder associated with human
XX molecules. They can be used to identify the presence of similar nucleic
XX acids. Dithp polynucleotides may be used to generate hybridisation probes
XX for use in chromosomal mapping. Polypeptides (DITHP) encoded by dithp are
XX used to screen for molecules which bind to them and modulate their
XX activity. Dithp polynucleotides can be used for gene therapy of disorders
XX such as severe combined immunodeficiency syndrome (SCID), cystic
XX fibrosis, thalassemia, haemophilia resulting from Factor VIII or IX
XX deficiencies, cardiovascular disorders e.g familial hypercholesterolaemia
XX (FH), cell proliferative disorders e.g. cancers, neurodegenerative
XX disorders, autoimmune/inflammatory disorders, infectious disorders and
XX developmental disorders. The antibodies can be used to analyse protein
XX expression levels

XX Sequence 499 BP; 107 A; 134 C; 189 G; 69 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.63e-06 Length: 499
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-09-827-854A-13 (1-18) x AAS03049 (1-499)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 128 ATGAAGGTTCTGTGGCTGCTGTGTCTACATCTCTGGCAGGATGCCAGGCC 181

RESULT 15

ABZ11994

ID ABZ11994 standard; cDNA; 583 BP.

XX ABZ11994;

AC ABZ11994;

XX 20-JAN-2003 (first entry)

XX Human polynucleotide SEQ ID NO 876.

XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
XX cell-proliferative disorder; neurodegenerative disease; bacterial;
XX Parkinson's disease; Alzheimer's disease; autoimmune disease;
XX multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
XX arthritis; cytostatic; immunomodulator; nontropic; neuroprotective;
XX antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
XX haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
XX antiarthritic; gene; ss.

OS Homo sapiens.

XX WO200270539-A2.

XX 12-SEP-2002.

XX 05-MAR-2002; 2002WO-US005095.

XX 05-MAR-2001; 2001US-00799451.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
XX Wehrman T, Wang J, Wang D, Drmanac RT;

XX WPI; 2002-759812/82.

XX P-ESDB; ABP69777.

XX New polynucleotides comprising sequences assembled from expressed
XX sequence tags (ESTs), useful for treating cell-proliferative,
XX neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
XX or coagulation disorders.

XX Claim 1; SEQ ID NO 876; 1012pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
XX nucleotide sequence selected from any of 948 sequences (ABZ11119-
XX ABZ12066) or their mature protein coding portion, active domain coding
XX protein or complementary sequences. The polynucleotides are useful for
XX identifying expressed genes or for physical mapping of human genome. The
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
XX markers, as a food supplement, for generating antibodies, in medical
XX imaging, screening and diagnostic assays and for treating cell-
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
XX or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
XX diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
XX platelet or coagulation disorders, wound, burns, incision, ulcers, liver
XX or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
XX arthritis, etc. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 583 BP; 138 A; 154 C; 161 G; 130 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.36e-06 Length: 583
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x ABZ11994 (1-583)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 56 ATGAAGGTTCTGTGGCTGCTGTGTCTACATCTCTGGCAGGATGCCAGGCC 109

Search completed: June 14, 2006, 19:10:36

Job time : 64.9495 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 19:02:39 ; Search time 476.517 Seconds

(without alignments)
3168.451 Million cell updates/sec

Title: US-09-827-854A-13

Perfect score: 92

Sequence: 1 MKVLWAAALLVFLAGCQA 18

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 segs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h
-USER=US09827854@cgn_1_17986 @runat_14062006_081827_26762 -NCPU=6 -ICPU=3
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

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2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_hcc.*
7: gb_est2.*
8: gb_est7.*
9: gb_est8.*
10: gb_est9.*
11: gb_gss1.*
12: gb_gss2.*
13: gb_gss3.*
14: gb_gss4.*

RESULT 1
CN277418
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
PUBMED
COMMENT

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	125	8	CN277418 170004177
2	92	100.0	177	2	BF877359 QV2-ET010
3	92	100.0	216	8	CN277422 170006000
4	92	100.0	221	2	BF877229 QV2-ET010

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C	5	92	100.0	221	2	BF877344	QV2-ET010
C	6	92	100.0	223	2	BF876758	QV2-ET010
C	7	92	100.0	223	2	BF877285	QV2-ET010
	8	92	100.0	227	2	BI039120	IL3-NT028
	9	92	100.0	230	2	BI040603	IL3-NT028
	10	92	100.0	243	8	CN277423	170004252
	11	92	100.0	256	7	BE164869	QV1-HT047
	12	92	100.0	256	7	BE164912	QV1-HT047
	13	92	100.0	269	4	CB153811	K-EST0211
	14	92	100.0	273	2	BF877186	QV2-ET010
	15	92	100.0	274	2	BF877232	QV2-ET010
	16	92	100.0	288	8	CN277389	170004248
C	17	92	100.0	293	7	BE766766	IL3-NT010
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	19	92	100.0	331	8	CN277408	170005319
	20	92	100.0	333	1	AI910041	RC-BT234
	21	92	100.0	343	8	CN277368	170005977
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	23	92	100.0	345	7	AW383864	QV3-HT036
	24	92	100.0	359	8	CN277382	170005325
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	26	92	100.0	364	8	CN277413	170005315
	27	92	100.0	372	3	BP418358	BP418358
	28	92	100.0	375	3	BQ684487	AGENCOURT
	29	92	100.0	377	10	DV770547	ILLUMIGEN
C	30	92	100.0	381	1	AA769671	ob19c01.8
	31	92	100.0	381	1	AV685514	AV685514
	32	92	100.0	382	1	AV686644	AV686644
C	33	92	100.0	383	1	AI347700	qp01f11.x
	34	92	100.0	384	1	AV683676	AV683676
	35	92	100.0	385	8	CN277384	170005316
	36	92	100.0	386	8	CN277411	170005315
C	37	92	100.0	387	1	AI310395	qo72b08.x
C	38	92	100.0	387	1	AI311109	qo92a10.x
	39	92	100.0	387	8	CN277371	170004554
	40	92	100.0	393	1	AV685887	AV685887
C	41	92	100.0	395	1	AI126876	qb95c05.x
	42	92	100.0	395	1	AV684377	AV684377
	43	92	100.0	397	8	CN277400	170006001
C	44	92	100.0	398	1	AI075319	ou65h09.x
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ALIGNMENTS

CN277418 17000417761214 GRN_EB Homo sapiens cDNA 5', mRNA linear EST 16-MAY-2004

CN277418 17000417761214 GRN_EB Homo sapiens cDNA 5', mRNA linear EST 16-MAY-2004

CN277418.1 GI:47293832

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 125)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,

L.Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,

Lebkowski, J. and Stanton, L.W.

Transcriptome characterization elucidates signaling networks that

control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Genon Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@genon.com

Insert Length: 125 Std Error: 0.00.

FEATURES
source

Location/Qualifiers
1. .125
/organism="Homo sapiens"
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/clone_lib="GRN EB"
/notes="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from HES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN

Alignment Scores:
Pred. No.: 6.07e-06 Length: 125
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservatives: 0
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Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-09-827-854A-13 (1-18) x CN277418 (1-125)

QY 1 MetLysValLeuTrpAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
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41 ATGAAGGTTCTGTGGGCTGGTGTGTGCACATTCCTGGCAGGATGCCAGGCC 94
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RESULT 2

BF877359 177 bp mRNA linear EST 17-JAN-2001
LOCUS QV2-ET0106-161100-475-f12 ET0106 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF877359
ACCESSION BF877359
VERSION BF877359.1 GI:12267489
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 177)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
PUBMED
COMMENT
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-
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High quality sequence stop: 177.

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FEATURES
source

Location/Qualifiers
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/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN EB"
/notes="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from HES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 9.21e-06 Length: 177
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-827-854A-13 (1-18) x BF877359 (1-177)

QY 1 MetLysValLeuTrpAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
|||||
24 ATGAAGGTTCTGTGGGCTGGTGTGTGCACATTCCTGGCAGGATGCCAGGCC 77
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RESULT 3

CN277422 216 bp mRNA linear EST 16-MAY-2004
LOCUS 17000600008337 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN277422
ACCESSION CN277422
VERSION CN277422.1 GI:47293836
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 216)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Pisk, G.J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Genon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8558
Fax: 650 473 7760
Email: rbrandenberger@genon.com
Insert Length: 216 Std Error: 0.00.

FEATURES

Location/Qualifiers
1. .216
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN PREHEP"
/notes="oligo dt primed, full-length enriched cDNA library
from DMSO-treated HES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Alignment Scores:
Pred. No.: 1.17e-05 Length: 216
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-09-827-854A-13 (1-18) x CN277422 (1-216)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
 |||||
 Db 54 ATGAAGGTTCTGTGGGCTGCTTGGTCACATCTCTGGCAGGATGCCAGGCC 107
 |||||
 RESULT 4
 BF877229/c
 LOCUS QV2-ET0106-151100-478-b01 ET0106 Homo sapiens cDNA, mRNA sequence. EST 17-JAN-2001
 DEFINITION BF877229
 ACCESSION BF877229
 VERSION BF877229.1 GI:12267359
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 221)
 AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Mateukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongenseel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-
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 High quality sequence stop: 221.
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 /db_xref="taxon:9606"
 /db_stage="Adult"
 /clone_lib="ET0106"
 /note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 ORIGIN
 Alignment Scores: 1.2e-05 Length: 221
 Pred. No.: 92.00 Matches: 18
 Score: 92.00
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0
 US-09-827-854A-13 (1-18) x BF877229 (1-221)
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 |||||
 Db 195 ATGAAGGTTCTGTGGGCTGCTTGGTCACATCTCTGGCAGGATGCCAGGCC 142
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 RESULT 5
 BF877344/c
 LOCUS QV2-ET0106-141100-474-g11 ET0106 Homo sapiens cDNA, mRNA sequence. EST 17-JAN-2001
 DEFINITION BF877344
 ACCESSION BF877344
 VERSION BF877344.1 GI:12267474
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 221)
 AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Mateukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongenseel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-
 141100-475-b06&t3=2000-11-16&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 221.
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 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /db_stage="Adult"
 /clone_lib="ET0106"
 /note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 ORIGIN
 Alignment Scores: 1.2e-05 Length: 221
 Pred. No.: 92.00 Matches: 18
 Score: 92.00
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0
 US-09-827-854A-13 (1-18) x BF877344 (1-221)
 Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
 |||||
 Db 195 ATGAAGGTTCTGTGGGCTGCTTGGTCACATCTCTGGCAGGATGCCAGGCC 142
 |||||

LOCUS QV2-ET0106-161100-475-b06 ET0106 Homo sapiens cDNA, mRNA sequence. EST 17-JAN-2001
 DEFINITION BF877344
 ACCESSION BF877344
 VERSION BF877344.1 GI:12267474
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 221)
 AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Mateukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongenseel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-
 161100-475-b06&t3=2000-11-16&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 221.
 FEATURES
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 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /db_stage="Adult"
 /clone_lib="ET0106"
 /note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 ORIGIN
 Alignment Scores: 1.2e-05 Length: 221
 Pred. No.: 92.00 Matches: 18
 Score: 92.00
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0
 US-09-827-854A-13 (1-18) x BF877344 (1-221)
 Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
 |||||
 Db 195 ATGAAGGTTCTGTGGGCTGCTTGGTCACATCTCTGGCAGGATGCCAGGCC 142
 |||||
 RESULT 6
 BF876758/c
 LOCUS QV2-ET0106-141100-474-g11 ET0106 Homo sapiens cDNA, mRNA sequence. EST 17-JAN-2001
 DEFINITION BF876758
 ACCESSION BF876758
 VERSION BF876758.1 GI:12266888
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 223)

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-
141100-474-g11&t3=2000-11-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 223.

FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0106"
/note="Organ: lung tumor; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Alignment Scores:
Pred. No.: 1 21e-05 Length: 223
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0
US-09-827-854A-13 (1-18) x BF876758 (1-223)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 197 ATGAAGGTTCTGTGGGCTGCTGCTGCATTCCTGGCAGATGCCAGGCC 144

RESULT 7
BF877285/c
LOCUS BF877285 223 bp mRNA linear EST 17-JAN-2001
DEFINITION QV2-ET0106-161100-474-g11 ET0106 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF877285
VERSION BF877285.1 GI:12267415
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 223)

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 223)

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-ET0106-
141100-474-g11&t3=2000-11-14&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 223.

FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0106"
/note="Organ: lung tumor; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Alignment Scores:
Pred. No.: 1 21e-05 Length: 223
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0
US-09-827-854A-13 (1-18) x BF877285 (1-223)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 197 ATGAAGGTTCTGTGGGCTGCTGCTGCATTCCTGGCAGATGCCAGGCC 144

RESULT 8
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LOCUS BI039120 227 bp mRNA linear EST 14-JUN-2001
DEFINITION IL3-NT0280-240101-418-F05 NT0280 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI039120
VERSION BI039120.1 GI:14445746
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 227)

REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed


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/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone_lib="GRN_ES"
/notes="oligo dr primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

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ORIGIN

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Alignment Scores:
Pred. No.: 1.35e-05 Length: 243
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

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US-09-827-854A-13 (1-18) x CN277423 (1-243)

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QY 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db 72 ATGAGGTTCTGTGGCTGGTTCACATTCCTGGCAGATGCCAGGCC 125
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RESULT 11

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BE164869
LOCUS BE164869 256 bp mRNA linear EST 21-JUN-2000
DEFINITION QV1-HT0471-270300-121-f07 HT0471 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE164869
VERSION BE164869.1 GI:8627590
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.K., Reis,L.F., de Souza,S.J. and Simpson,A.J.
1 (bases 1 to 256)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

```

```

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=QV1-HT0471-270
300-121-f07&t3=2000-03-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 256.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0471"
/notes="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of

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FEATURES

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/dev_stage="Adult"
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/notes="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of

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ORIGIN

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Alignment Scores:
Pred. No.: 1.43e-05 Length: 256
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

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US-09-827-854A-13 (1-18) x BE164869 (1-256)

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QY 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db 17 ATGAGGTTCTGTGGCTGGTTCACATTCCTGGCAGATGCCAGGCC 70
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RESULT 12

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BE164912
LOCUS BE164912 256 bp mRNA linear EST 21-JUN-2000
DEFINITION QV1-HT0471-280300-121-f07 HT0471 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE164912
VERSION BE164912.1 GI:8627633
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.K., Reis,L.F., de Souza,S.J. and Simpson,A.J.
1 (bases 1 to 256)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

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```

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=QV1-HT0471-280
300-121-f07&t3=2000-03-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 256.
Location/Qualifiers
1..256
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0471"
/notes="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of

```

ORIGIN

Alignment Scores:

Pred. No.: 1.43e-05 Length: 256
 Score: 92.00 Matches: 18
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-09-827-854A-13 (1-18) x BE164912 (1-256)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
 Db 17 ATGAAGGTTCTGTGGCTGCGTTCATTCCTGGCAGGATGCCAGGCC 70

RESULT 13

CB153811 269 bp mRNA linear EST 29-JAN-2003
 LOCUS K-EST0211405 L17N670205 Homo sapiens cDNA clone L17N670205-6-G09
 DEFINITION 5', mRNA sequence.

ACCESSION CB153811

VERSION CB153811.1 GI:28138807

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

1 (bases 1 to 269)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

CONTACT: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 6, row: G column: 09

High quality sequence stop: 269.

Location/Qualifiers

source

1. .269

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="L17N670205-6-G09"

/sex="F"

/lab host="Top10F"

/clone lib="L17N670205"

/note="Organ: Liver; Vector: pT73D-PacI; Site_1: EcoRI;
 Site_2: NotI; The library was contributed by the Soares
 laboratory and it was constructed as described by Bonaldo,
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
 6(9): 791-806. RNA was prepared from harvested cell
 culture."

ORIGIN

Alignment Scores:
 Pred. No.: 1.52e-05 Length: 269
 Score: 92.00 Matches: 18
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
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US-09-827-854A-13 (1-18) x CB153811 (1-269)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18

Db 45 ATGAAGGTTCTGTGGCTGCGTTCATTCCTGGCAGGATGCCAGGCC 98

RESULT 14

BF877186

LOCUS

DEFINITION QV2-ET0106-151100-477-f05 ET0106 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF877186

VERSION BF877186.1 GI:12267316

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 273)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.P., Matukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

Proc Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

PUBMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV2&t2-QV2-ET0106-

151100-477-f05&t3=2000-11-15&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 273.

FEATURES

source

1. .273

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev stage="Adult"

/clone lib="ET0106"

/note="Organ: lung tumor; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Alignment Scores:
 Pred. No.: 1.55e-05 Length: 273
 Score: 92.00 Matches: 18
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
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US-09-827-854A-13 (1-18) x BF877186 (1-273)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18

Db 25 ATGAAGGTTCTGTGGCTGCGTTCATTCCTGGCAGGATGCCAGGCC 78

RESULT 15

BF877232

LOCUS

DEFINITION BF877232 274 bp mRNA linear EST 17-JAN-2001

ACCESSION QV2-ET0106-151100-478-c04 ET0106 Homo sapiens cDNA, mRNA sequence.

VERSION BF877232

KEYWORDS BF877232.1 GI:12267362

EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 274)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=QV2&t2=QV2-ET0106-151100-478-c04&t3=2000-11-15&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 274.
 FEATURES
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 1..274
 Location/Qualifiers
 .organism="Homo sapiens"
 .mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="ET0106"
 notes="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORFESTS PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.55e-05 Length: 274
 Score: 92.00 Matches: 18
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0
 US-09-827-854A-13 (1-18) x BF877232 (1-274)
 Qy 1 MethysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
 Db 26 ATGAAGTCTCTGGGCTGGCTGCTGGTACATCTTCGACATTCCTGGCAGGATCCAGGCC 79

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 19:03:31 ; Search time 18.795 seconds
(without alignments)

2687.952 Million cell updates/sec

Title: US-09-827-854A-13

Perfect score: 92

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	71	2	US-08-148-910-10
2	92	100.0	71	2	US-08-448-937A-10
3	92	100.0	93	3	US-09-391-104-4
4	92	100.0	405	3	US-09-513-999C-2137
5	92	100.0	478	4	US-09-880-107-2491
6	92	100.0	583	3	US-09-789-451-876
7	92	100.0	660	2	US-08-726-306A-28
8	92	100.0	684	4	US-10-211-689-29

9	92	100.0	709	4	US-10-211-689-41	Sequence 41, Appl
10	92	100.0	718	4	US-10-211-689-35	Sequence 35, Appl
11	92	100.0	788	4	US-10-211-689-33	Sequence 33, Appl
12	92	100.0	802	4	US-10-211-689-31	Sequence 31, Appl
13	92	100.0	1156	3	US-09-023-655-1007	Sequence 1007, Ap
14	92	100.0	1157	2	US-07-709-949-1	Sequence 1, Appli
15	92	100.0	1157	4	US-09-880-107-2244	Sequence 2244, Ap
16	92	100.0	1291	3	US-09-919-039-246	Sequence 246, App
17	87	94.6	616	4	US-10-211-689-39	Sequence 39, Appl
18	87	94.6	691	4	US-10-211-689-45	Sequence 45, Appl
19	84	91.3	372	3	US-09-621-976-1386	Sequence 1386, Ap
20	75	81.5	3805	3	US-09-108-006C-3	Sequence 3, Appli
21	68	73.9	1126	3	US-08-949-155-5	Sequence 5, Appli
22	68	73.9	1126	3	US-09-819-964-5	Sequence 5, Appli
23	58	63.0	4267	3	US-08-949-155-51	Sequence 51, Appl
24	58	63.0	4267	3	US-09-819-964-51	Sequence 51, Appl
c 25	54	58.7	183	3	US-09-489-039A-7011	Sequence 7011, Ap
26	54	58.7	645	3	US-09-489-039A-7153	Sequence 7153, Ap
27	53	57.6	303	3	US-09-252-991A-2604	Sequence 2604, Ap
c 28	53	57.6	6285	3	US-09-949-016-12815	Sequence 12815, A
c 29	53	57.6	6286	3	US-09-949-016-17179	Sequence 17179, A
c 30	53	57.6	6794	3	US-09-902-540-736	Sequence 736, App
31	50	54.3	1143	3	US-09-902-540-3531	Sequence 3531, Ap
c 32	50	54.3	18538	3	US-09-902-540-1169	Sequence 1169, Ap
c 33	48.5	52.7	367	3	US-09-513-999C-2304	Sequence 2304, Ap
34	48	52.2	3909	2	US-08-232-537-1	Sequence 1, Appli
35	47	51.1	576	3	US-09-252-991A-9976	Sequence 9976, Ap
c 36	47	51.1	670689	3	US-09-949-016-12505	Sequence 12505, A
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38	46	50.0	601	3	US-09-949-016-197665	Sequence 197665,
39	46	50.0	2665	3	US-09-902-540-3712	Sequence 3712, A
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c 44	45.5	49.5	57507	3	US-09-949-016-15019	Sequence 15019, A
c 45	45	48.9	438	3	US-09-902-540-1579	Sequence 1579, Ap

ALIGNMENTS

RESULT 1

US-08-148-910-10

; Sequence 10, Application US/08148910

; Patent No. 5466593

; GENERAL INFORMATION:

; APPLICANT: Takeshi SHIMOMURA et al.

; TITLE OF INVENTION: No. 5466593el Protein and Gene Encoding Said Protein

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch,

; MEDIUM TYPE: 500 Kb Storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/148,910

; FILING DATE: No. 5466593ember 5, 1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 71 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid (synthetic DNA)

ORIGINAL SOURCE:

ORGANISM: human

US-08-148-910-10

Alignment Scores:
Pred. No.: 1.54e-08 Length: 71
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-827-854A-13 (1-18) x US-08-148-910-10 (1-71)

QY 1 MetLysValLeuTrpAlaLaLeuValThrPheLeuAlaGlyCysGlnAla 18
DB 12 ATGAAGGTTCTGTGGGCTGGTGTGGTGCACATTCTTGGCAGGATGCCAGGCC 65

RESULT 2

US-08-448-937A-10

Sequence 10, Application US/08448937A

Patent No. 5677164

GENERAL INFORMATION:

APPLICANT: Takeshi SHIMOMURA et al.

TITLE OF INVENTION: No. 5677164el Protein and Gene Encoding Said Protein

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch,

MEDIUM TYPE: 500 Kb Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/448,937A

FILING DATE: May 24, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/148,910

FILING DATE: No. 5677164ember 5, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX: 202-371-8856

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 71 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid (synthetic DNA)

ORIGINAL SOURCE:

ORGANISM: human

US-08-448-937A-10

Alignment Scores:

Pred. No.: 1.54e-08 Length: 71

Score: 92.00 Matches: 18

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 2 Gaps: 0

US-09-827-854A-13 (1-18) x US-08-448-937A-10 (1-71)

QY 1 MetLysValLeuTrpAlaLaLeuValThrPheLeuAlaGlyCysGlnAla 18
DB 12 ATGAAGGTTCTGTGGGCTGGTGTGGTGCACATTCTTGGCAGGATGCCAGGCC 65

RESULT 3

US-09-391-104-4

Sequence 4, Application US/09391104

Patent No. 6399371

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Falduto, Michael T.

APPLICANT: Magnuson, Scott R.

APPLICANT: Morgan, Douglas W.

TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,

TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS

TITLE OF INVENTION: OF USING SAME

FILE REFERENCE: 6073.US.P1

CURRENT APPLICATION NUMBER: US/09/391,104

CURRENT FILING DATE: 1999-09-07

PRIOR APPLICATION NUMBER: US 08/814,394

PRIOR FILING DATE: 1997-03-11

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 93

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Upstream primer

US-09-391-104-4

Alignment Scores:

Pred. No.: 2.13e-08 Length: 93

Score: 92.00 Matches: 18

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-09-827-854A-13 (1-18) x US-09-391-104-4 (1-93)

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DB 16 ATGAAGGTTCTGTGGGCTGGTGTGGTGCACATTCTTGGCAGGATGCCAGGCC 69

RESULT 4

US-09-513-999C-2137

Sequence 2137, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59.US2.9961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26


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; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,306A
; FILING DATE: 02-Oct-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 95/20080.4
; FILING DATE: 02-Oct-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/009,832
; FILING DATE: 01-Jan-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-726-306A-28

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Alignment Scores:
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

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US-09-827-854A-13 (1-18) x US-08-726-306A-28 (1-660)

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RESULT 8
US-10-211-689-29
; Sequence 29, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
; APPLICANT: Aleobrook, John II
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Khrantsov, Nikolai V.
; APPLICANT: Lepley, Denise M.
; APPLICANT: MacDougall, John R.
; APPLICANT: Pena, Carol A.
; APPLICANT: Peyman, John A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Spyttek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

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; FILE REFERENCE: 21402-416B
; CURRENT APPLICATION NUMBER: US/10/211,689
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/311751
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/310,802
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,795
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/361,159
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/373,050
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/380,970
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/381,030
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/323,944
; PRIOR FILING DATE: 2001-09-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 29
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(599)
US-10-211-689-29

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Alignment Scores:
Pred. No.: 2,38e-07 Length: 684
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

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US-09-827-854A-13 (1-18) x US-10-211-689-29 (1-684)

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Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
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Db 18 ATGAAGTTCTGTGGGCTGGTGTGCATTCCTGCGAGGATGCCAGGCC 71
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RESULT 9
US-10-211-689-41
; Sequence 41, Application US/10211689
; Patent No. 6974684
; GENERAL INFORMATION:
; APPLICANT: Aleobrook, John II
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Khrantsov, Nikolai V.
; APPLICANT: Lepley, Denise M.
; APPLICANT: MacDougall, John R.
; APPLICANT: Pena, Carol A.
; APPLICANT: Peyman, John A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Spyttek, Kimberly A.

```


; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-416B

; CURRENT APPLICATION NUMBER: US/10/211,689

; CURRENT FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: 60/311,751

; PRIOR FILING DATE: 2001-08-10

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

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; PRIOR FILING DATE: 2001-08-08

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; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

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; PRIOR FILING DATE: 2001-08-08

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; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; PRIOR FILING DATE: 2001-08-08

; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH

; FILE REFERENCE: 21402-416B

; CURRENT APPLICATION NUMBER: US/10/211,689

; CURRENT FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: 60/311,751

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/310,802

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/310,795

; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/311,292

; PRIOR FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 60/361,159

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: 60/373,050

; PRIOR FILING DATE: 2002-04-16

; PRIOR APPLICATION NUMBER: 60/380,970

; PRIOR FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: 60/311,979

; PRIOR FILING DATE: 2001-08-13

; PRIOR APPLICATION NUMBER: 60/381,030

; PRIOR FILING DATE: 2002-05-16

; PRIOR APPLICATION NUMBER: 60/323,944

; PRIOR FILING DATE: 2001-09-21

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 132

; SOFTWARE: Curaseqlist version 0.1

; SEQ ID NO 35

; LENGTH: 718

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2)..(718)

; US-10-211-689-35

Alignment Scores:

Pred. No.: 2.52e-07

Score: 92.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 100.0%

DB: 4

Length: 718

Matches: 18

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-827-854A-13 (1-18) x US-10-211-689-35 (1-718)

Qy 1 MetlysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18

Db 11 ATGAAGGTTCTGTGGGCTGGCTGCTGCATCTCTGGCAGGATGCCAGGCC 64

RESULT 11

US-10-211-689-33

; Sequence 33, Application US/10211689

; Patent No. 6974684

; GENERAL INFORMATION:

; APPLICANT: Alsbrook, John II

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gangolli, Esha A.

; APPLICANT: Gorman, Linda

; APPLICANT: Guo, Xiaojia (Sasha)

; APPLICANT: Khrastov, Nikolai V.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Meera

; APPLICANT: Meera

; APPLICANT: Meera

; APPLICANT: Meera

; APPLICANT: Meera

; APPLICANT: Meera

; APPLICANT: Meera

APPLICANT: MacDougall, John R.
APPLICANT: Pena, Carol A.
APPLICANT: Peyman, John A.
APPLICANT: Patturajan, Meera
APPLICANT: Rieger, Daniel K.
APPLICANT: Shimkets, Richard A.
APPLICANT: Smithson, Glenda
APPLICANT: Spyttek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Voss, Edward Z.
APPLICANT: Zhong, Mei

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-416B

CURRENT APPLICATION NUMBER: US/10/211,689

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: 60/311751

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/310,802

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: 60/310,795

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: 60/311,292

PRIOR FILING DATE: 2001-08-09

PRIOR APPLICATION NUMBER: 60/361,159

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 60/373,050

PRIOR FILING DATE: 2002-04-16

PRIOR APPLICATION NUMBER: 60/380,970

PRIOR FILING DATE: 2002-05-15

PRIOR APPLICATION NUMBER: 60/311,979

PRIOR FILING DATE: 2001-08-13

PRIOR APPLICATION NUMBER: 60/381,030

PRIOR FILING DATE: 2002-05-16

PRIOR APPLICATION NUMBER: 60/323,944

PRIOR FILING DATE: 2001-09-21

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 132

SOFTWARE: Curaseqlist version 0.1

SEQ ID NO 33

LENGTH: 788

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (18)..(704)

US-10-211-689-33

Alignment Scores:
Pred. No.: 2.82e-07 Length: 788
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-211-689-33 (1-788)

Qy 1 MetLysValLeuTrpAlaLeuValThrPheLeuAlaGlyCysGlnAla 18

Db 18 ATGAAGGTTCTGTGGGCTGCTGTCACATTCTTGGCAGGATGCCAGGCC 71

RESULT 12

US-10-211-689-31

Sequence 31, Application US/10211689

Patent No. 6974684

GENERAL INFORMATION:

APPLICANT: Alcobrook, John II

APPLICANT: Anderson, David W.

APPLICANT: Boldog, Ferenc L.

APPLICANT: Burgess, Catherine E.

APPLICANT: Casman, Stacie J.

APPLICANT: Edinger, Shlomik R.

APPLICANT: Gangolli, Esha A.

APPLICANT: Gorman, Linda
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Khrastov, Nikolai V.
APPLICANT: Lepley, Denise M.
APPLICANT: MacDougall, John R.
APPLICANT: Pena, Carol A.
APPLICANT: Peyman, John A.
APPLICANT: Patturajan, Meera
APPLICANT: Rieger, Daniel K.
APPLICANT: Shimkets, Richard A.
APPLICANT: Smithson, Glenda
APPLICANT: Spyttek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Voss, Edward Z.
APPLICANT: Zhong, Mei

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-416B

CURRENT APPLICATION NUMBER: US/10/211,689

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: 60/311751

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/310,802

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: 60/310,795

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: 60/311,292

PRIOR FILING DATE: 2001-08-09

PRIOR APPLICATION NUMBER: 60/361,159

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 60/373,050

PRIOR FILING DATE: 2002-04-16

PRIOR APPLICATION NUMBER: 60/380,970

PRIOR FILING DATE: 2002-05-15

PRIOR APPLICATION NUMBER: 60/311,979

PRIOR FILING DATE: 2001-08-13

PRIOR APPLICATION NUMBER: 60/381,030

PRIOR FILING DATE: 2002-05-16

PRIOR APPLICATION NUMBER: 60/323,944

PRIOR FILING DATE: 2001-09-21

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 132

SOFTWARE: Curaseqlist version 0.1

SEQ ID NO 31

LENGTH: 802

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (18)..(716)

US-10-211-689-31

Alignment Scores:
Pred. No.: 2.88e-07 Length: 802
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-211-689-31 (1-802)

Qy 1 MetLysValLeuTrpAlaLeuValThrPheLeuAlaGlyCysGlnAla 18

Db 18 ATGAAGGTTCTGTGGGCTGCTGTCACATTCTTGGCAGGATGCCAGGCC 71

RESULT 13

US-09-023-655-1007

Sequence 1007, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Seilhamer

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; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1007:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1156 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: gi78850
; US-09-023-655-1007

Alignment Scores:
Pred. No.: 4.48e-07 Length: 1156
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-13 (1-18) x US-09-023-655-1007 (1-1156)

QY 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 61 ATGAAGGTCTGTGGGCTGGTGTGGTGCACATTCCTGGCAGGATGCCAGGCC 114

RESULT 14
US-07-709-949-1
; Sequence 1, Application US/07709949
; Patent No. 5472858
; GENERAL INFORMATION:
; APPLICANT: Attie, Alan D
; APPLICANT: Gretch, Daniel G
; APPLICANT: Sturley, Stephen L
; APPLICANT: Beckage, Nancy E
; TITLE OF INVENTION: Production of Recombinant Proteins in
; TITLE OF INVENTION: Insect Larvae
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: P.O. Box 2113
; CITY: Madison
; STATE: WI
; COUNTRY: USA

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; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2244
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 M12529
US-09-880-107-2244

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Alignment Scores:
Pred. No.:      4.49e-07      Length:      1157
Score:          92.00      Matches:      18
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:      100.0%      Indels: 0
DB:               4          Gaps: 0

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US-09-827-854A-13 (1-18) x US-09-880-107-2244 (1-1157)

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Db      62 ATGAGGTTCTGTGGGCTGCTGTGTGCACATCTCTGCAGGATGCCAGGCC 115

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Search completed: June 14, 2006, 19:16:12
Job time : 20.795 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 21:46:34 ; Search time 129.918 Seconds
(without alignments)
2553.658 Million cell updates/sec

Title: US-09-827-854A-13
Perfect score: 92
Sequence: 1 MKVLWAALLVTLACQCA 18

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Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA Main -QFMT=fastcap -SUFFIX=p2n.rnpbm
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-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPWT=pt0 -NORM=ext
-HEAPSIZES=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h
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-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6 -FCGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:
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4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
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14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
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2	92	100.0	201	8	US-10-741-601-3278	Sequence 3278, Ap
3	92	100.0	201	10	US-10-995-561-8950	Sequence 8950, Ap
4	92	100.0	407	3	US-09-823-245A-7	Sequence 7, Appli
5	92	100.0	440	9	US-10-696-639-2937	Sequence 2937, Ap
6	92	100.0	441	3	US-10-696-639-2936	Sequence 2936, Ap
7	92	100.0	445	3	US-09-918-995-8875	Sequence 8875, Ap
8	92	100.0	478	3	US-09-964-824A-374	Sequence 374, App
c	92	100.0	478	3	US-09-880-107-2491	Sequence 2491, Ap
c	92	100.0	478	3	US-09-873-367C-1016	Sequence 1016, Ap
c	92	100.0	478	10	US-10-843-641A-1016	Sequence 1016, Ap
c	92	100.0	478	10	US-10-843-641A-5677	Sequence 5677, Ap
13	92	100.0	583	8	US-10-302-172-876	Sequence 876, App
14	92	100.0	684	7	US-10-211-689-29	Sequence 29, Appl
15	92	100.0	709	7	US-10-211-689-41	Sequence 41, Appl
16	92	100.0	718	7	US-10-211-689-35	Sequence 35, Appl
17	92	100.0	788	7	US-10-211-689-33	Sequence 33, Appl
18	92	100.0	802	7	US-10-211-689-31	Sequence 31, Appl
19	92	100.0	1147	7	US-10-257-021-63	Sequence 63, Appl
20	92	100.0	1156	3	US-09-827-854-7	Sequence 7, Appli
21	92	100.0	1156	3	US-09-827-854-8	Sequence 8, Appli
22	92	100.0	1156	3	US-09-827-854-9	Sequence 9, Appli
23	92	100.0	1156	3	US-09-827-854-10	Sequence 10, Appl
24	92	100.0	1156	3	US-09-827-854-11	Sequence 11, Appl
25	92	100.0	1156	3	US-09-827-854-12	Sequence 12, Appl
26	92	100.0	1156	3	US-09-870-759-129	Sequence 129, App
27	92	100.0	1156	3	US-09-802-640-17	Sequence 17, Appl
28	92	100.0	1156	3	US-09-751-708A-129	Sequence 129, App
29	92	100.0	1156	7	US-10-301-822-5	Sequence 5, Appli
30	92	100.0	1156	7	US-10-313-641-1	Sequence 1, Appli
31	92	100.0	1156	7	US-10-403-902A-17	Sequence 17, Appl
32	92	100.0	1156	7	US-10-428-551-1	Sequence 1, Appli
33	92	100.0	1156	8	US-10-641-643-1007	Sequence 1007, Ap
34	92	100.0	1156	9	US-10-428-817A-125	Sequence 125, App
35	92	100.0	1156	9	US-10-794-198A-1	Sequence 1, Appli
36	92	100.0	1156	10	US-10-852-335A-10	Sequence 10, Appl
37	92	100.0	1156	10	US-10-937-758A-106	Sequence 106, App
38	92	100.0	1156	10	US-10-773-446-63	Sequence 63, Appl
39	92	100.0	1156	15	US-11-186-284-5	Sequence 5, Appli
40	92	100.0	1156	15	US-11-055-309A-1	Sequence 1, Appli
41	92	100.0	1157	3	US-09-954-456-760	Sequence 760, App
42	92	100.0	1157	3	US-09-880-107-2244	Sequence 2244, Ap
43	92	100.0	1157	3	US-09-960-706-655	Sequence 655, App
44	92	100.0	1157	3	US-09-873-319-409	Sequence 409, App
45	92	100.0	1157	7	US-10-313-641-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-391-104-4
; Sequence 4, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; PRIOR FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; NUMBER OF SEQ ID NOS: 35
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Upstream primer

US-09-391-104-4

Alignment Scores:
Pred. No.: 4,91e-07 Length: 93
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-13 (1-18) x US-09-391-104-4 (1-93)

QY 1 MetLysValLeuTrpAlaAlaLeuValThrpheLeuAlaGlyCysGlnAla 18
DB 16 ATGAAGGTTCTGTGGGCTGGCTGGTTCACATTCTGGCAGGATGCCAGGCC 69

RESULT 2

US-10-741-601-3278
; Sequence 3278, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 28415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3278
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-3278

Alignment Scores:
Pred. No.: 1.18e-06 Length: 201
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-741-601-3278 (1-201)

QY 1 MetLysValLeuTrpAlaAlaLeuValThrpheLeuAlaGlyCysGlnAla 18
DB 11 ATGAAGGTTCTGTGGGCTGGCTGGTTCACATTCTGGCAGGATGCCAGGCC 64

RESULT 3

US-10-995-561-8950
; Sequence 8950, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8950
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-8950

Alignment Scores:
Pred. No.: 1.18e-06 Length: 201
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-995-561-8950 (1-201)

QY 1 MetLysValLeuTrpAlaAlaLeuValThrpheLeuAlaGlyCysGlnAla 18
DB 11 ATGAAGGTTCTGTGGGCTGGCTGGTTCACATTCTGGCAGGATGCCAGGCC 64

RESULT 4

US-09-823-245A-7
; Sequence 7, Application US/09823245A
; Publication No. US20020039760A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fachtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823,245A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/194,941
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-7

Alignment Scores:
Pred. No.: 2.63e-06 Length: 407
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-13 (1-18) x US-09-823-245A-7 (1-407)

QY 1 MetLysValLeuTrpAlaAlaLeuValThrpheLeuAlaGlyCysGlnAla 18
DB 20 ATGAAGGTTCTGTGGGCTGGCTGGTTCACATTCTGGCAGGATGCCAGGCC 73

RESULT 5

US-10-696-639-2937
; Sequence 2937, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bourner, Maureen J.
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2937
; LENGTH: 440
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:

; NAME/KEY: misc feature
; LOCATION: (339)..(412)
; OTHER INFORMATION: n=unknown
US-10-696-639-2937

Alignment Scores:
Pred. No.: 2.87e-06 Length: 440
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-696-639-2937 (1-440)

Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 57 ATGAAGGTTCTGTGGCTGCGTTGCTGTCACATTCCTGGCAGGATGCCAGGCC 110

RESULT 6

US-10-696-639-2936
; Sequence 2936, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; TITLE OF INVENTION: DIFFERENTIALY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2936
; LENGTH: 441
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-696-639-2936

Alignment Scores:
Pred. No.: 2.88e-06 Length: 441
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-696-639-2936 (1-441)

Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 56 ATGAAGGTTCTGTGGCTGCGTTGCTGTCACATTCCTGGCAGGATGCCAGGCC 109

RESULT 7

US-09-918-995-8875
; Sequence 8875, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8875
; LENGTH: 445
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(445)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8875

Alignment Scores:
Pred. No.: 2.91e-06 Length: 445
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-13 (1-18) x US-09-918-995-8875 (1-445)

Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 169 ATGAAGGTTCTGTGGCTGCGTTGCTGTCACATTCCTGGCAGGATGCCAGGCC 222

RESULT 8

US-09-964-824A-374/c
; Sequence 374, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 374
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(478)
; OTHER INFORMATION: n=a,t,g or c
US-09-964-824A-374

Alignment Scores:
Pred. No.: 3.16e-06 Length: 478
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-13 (1-18) x US-09-964-824A-374 (1-478)

Qy 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 396 ATGAAGGTTCTGTGGCTGCGTTGCTGTCACATTCCTGGCAGGATGCCAGGCC 343

RESULT 9

US-09-880-107-2491/c
; Sequence 2491, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.

;/ TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;/ FILE REFERENCE: 44921-5028-WO
;/ CURRENT APPLICATION NUMBER: US/09/880,107
;/ CURRENT FILING DATE: 2001-06-14
;/ PRIOR APPLICATION NUMBER: US 60/211,379
;/ PRIOR FILING DATE: 2000-06-14
;/ PRIOR APPLICATION NUMBER: US 60/237,054
;/ PRIOR FILING DATE: 2000-10-02
;/ NUMBER OF SEQ ID NOS: 3950
;/ SOFTWARE: PatentIn Ver. 2.1
;/ SEQ ID NO 2491
;/ LENGTH: 478
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ OTHER INFORMATION: Genbank Accession No. US20020142981A1 N33009
;/ NAME/KEY: unsure
;/ LOCATION: (1)..(478)
;/ OTHER INFORMATION: n = a or c or g or t
US-09-880-107-2491

Alignment Scores:
Pred. No.: 3.16e-06 Length: 478
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-13 (1-18) x US-09-880-107-2491 (1-478)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
|||||
Db 396 ATGAAGGTTCTGTGGCTGCGTTCACATTCTTCGAGGATGCCAGGCC 343

RESULT 10
US-09-873-367C-1016/c
;/ Sequence 1016, Application US/09873367C
;/ Publication No. US20030165839A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Young, Paul
;/ APPLICANT: Soppet, Daniel
;/ APPLICANT: Endress, Gregory
;/ APPLICANT: Augustus, Meena
;/ APPLICANT: Ebner, Reinhard
;/ APPLICANT: Carter, Kenneth
;/ TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;/ FILE REFERENCE: 689290-64
;/ CURRENT APPLICATION NUMBER: US/09/873,367C
;/ CURRENT FILING DATE: 2003-04-29
;/ PRIOR APPLICATION NUMBER: U.S. 60/236,891
;/ PRIOR FILING DATE: 2000-09-29
;/ PRIOR APPLICATION NUMBER: U.S. 60/236,842
;/ PRIOR FILING DATE: 2000-09-29
;/ PRIOR FILING DATE: 2000-11-01
;/ PRIOR APPLICATION NUMBER: U.S. 60/244,867
;/ PRIOR FILING DATE: 2000-11-01
;/ PRIOR APPLICATION NUMBER: U.S. 60/245,084
;/ PRIOR FILING DATE: 2000-11-01
;/ NUMBER OF SEQ ID NOS: 1067
;/ SOFTWARE: PatentIn version 3.0
;/ SEQ ID NO 1016
;/ LENGTH: 478
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ NAME/KEY: misc_feature
;/ LOCATION: (1)..(478)
;/ OTHER INFORMATION: n=a,t,g or c
US-09-873-367C-1016

Alignment Scores:
Pred. No.: 3.16e-06 Length: 478

Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-827-854A-13 (1-18) x US-09-873-367C-1016 (1-478)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
|||||
Db 396 ATGAAGGTTCTGTGGCTGCGTTCACATTCTTCGAGGATGCCAGGCC 343

RESULT 11

US-10-843-641A-1016/c
;/ Sequence 1016, Application US/10843641A
;/ Publication No. US20050064454A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Avalon Pharmaceuticals, Inc.
;/ TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;/ FILE REFERENCE: 689290-189
;/ CURRENT APPLICATION NUMBER: US/10/843,641A
;/ CURRENT FILING DATE: 2004-05-12
;/ PRIOR APPLICATION NUMBER: US/09/873,367
;/ PRIOR FILING DATE: 2001-06-05
;/ PRIOR APPLICATION NUMBER: US/09/954,531
;/ PRIOR FILING DATE: 2001-09-18
;/ PRIOR APPLICATION NUMBER: US/09/954,456
;/ PRIOR FILING DATE: 2001-09-25
;/ PRIOR APPLICATION NUMBER: US/09/962,436
;/ PRIOR FILING DATE: 2001-09-25
;/ PRIOR APPLICATION NUMBER: US/09/962,832
;/ PRIOR FILING DATE: 2001-09-25
;/ PRIOR APPLICATION NUMBER: US/09/964,824
;/ PRIOR FILING DATE: 2001-09-27
;/ PRIOR APPLICATION NUMBER: US/09/967,768
;/ PRIOR FILING DATE: 2001-09-28
;/ PRIOR APPLICATION NUMBER: US/09/968,007
;/ PRIOR FILING DATE: 2001-10-02
;/ PRIOR APPLICATION NUMBER: US/09/969,347
;/ PRIOR FILING DATE: 2001-10-02
;/ PRIOR APPLICATION NUMBER: US/09/969,708
;/ PRIOR FILING DATE: 2001-10-03
;/ Remaining Prior Application data removed - See File Wrapper or PALM.
;/ NUMBER OF SEQ ID NOS: 8447
;/ SOFTWARE: PatentIn version 3.0
;/ SEQ ID NO 1016
;/ LENGTH: 478
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ NAME/KEY: misc_feature
;/ LOCATION: (1)..(478)
;/ OTHER INFORMATION: n=a,t,g or c
US-10-843-641A-1016

Alignment Scores:
Pred. No.: 3.16e-06 Length: 478
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-843-641A-1016 (1-478)

Qy 1 MetLysValLeuTrpAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
|||||
Db 396 ATGAAGGTTCTGTGGCTGCGTTCACATTCTTCGAGGATGCCAGGCC 343

RESULT 12

US-10-843-641A-5677/c
;/ Sequence 5677, Application US/10843641A

Publication No. US20050064454A1
GENERAL INFORMATION:
APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-189
CURRENT APPLICATION NUMBER: US/10/843,641A
CURRENT FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: US/09/873,367
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US/09/954,531
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/09/954,456
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,436
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,832
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/964,824
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/09/967,768
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/968,007
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,347
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,708
PRIOR FILING DATE: 2001-10-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 8447
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5677
LENGTH: 478
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(478)
OTHER INFORMATION: n=a,t,g or c
US-10-843-641A-5677

Alignment Scores:
Pred. No.: 3.16e-06 Length: 478
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0
US-09-827-854A-13 (1-18) x US-10-843-641A-5677 (1-478)

Qy 1 MetLysValLeuTrpAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 396 ATGAAGGTTCTGTGGCTGCGTGTGTCACATTCTCGCAGGATGCCAGGCC 343

RESULT 13

US-10-302-172-876
Sequence 876, Application US/10302172
Publication No. US20040053250A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids an
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803 1CNCp
CURRENT APPLICATION NUMBER: US/10/302,172
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/799,451

PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 950
SOFTWARE: pc_fl_genes Version 2.0
SEQ ID NO 876
LENGTH: 583
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (100)..(423)
US-10-302-172-876
Alignment Scores:
Pred. No.: 3.96e-06 Length: 583
Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0
US-09-827-854A-13 (1-18) x US-10-302-172-876 (1-583)

Qy 1 MetLysValLeuTrpAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 56 ATGAAGGTTCTGTGGCTGCGTGTGTCACATTCTCGCAGGATGCCAGGCC 109

RESULT 14

US-10-211-689-29
Sequence 29, Application US/10211689
Publication No. US20030232347A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, John II
APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie J.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gorman, Linda
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Khrantsov, Nikolai V.
APPLICANT: Lepley, Denise M.
APPLICANT: MacDougall, John R.
APPLICANT: Pena, Carol A.
APPLICANT: Peyman, John A.
APPLICANT: Patturajan, Meera
APPLICANT: Rieger, Daniel K.
APPLICANT: Shinkets, Richard A.
APPLICANT: Smithson, Glennnda
APPLICANT: Spytek, Kimberly A.
APPLICANT: Vernet, Corine A. M.
APPLICANT: Voss, Edward Z.
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
FILE REFERENCE: 21402-416B
CURRENT APPLICATION NUMBER: US/10/211,689
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 60/311751
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/310,802
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,795
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/361,159
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/373,050
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/380,970
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 60/311,979

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; PRIOR APPLICATION NUMBER: 60/381,030
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/323,944
; PRIOR FILING DATE: 2001-09-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 29
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(599)
US-10-211-689-29

Alignment Scores:
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Score: 92.00 Matches: 18
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-211-689-29 (1-684)

Qy 1 MetLysValLeuTrpAlaLaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 18 ATGAAGGTTCTGTGGGCTGCTGTGTCACATTCTGCGAGGATGCCAGGCC 71

RESULT 15
US-10-211-689-41
; Sequence 41, Application US/10211689
; Publication No. US20030232347A1
; GENERAL INFORMATION:
; APPLICANT: Alsebrook, John II
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaofia (Sasha)
; APPLICANT: Khrantsov, Nikolai V.
; APPLICANT: Lepley, Denise M.
; APPLICANT: McDougall, John R.
; APPLICANT: Pena, Carol A.
; APPLICANT: Peyman, John A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-4168
; CURRENT APPLICATION NUMBER: US/10/211,689
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/311751
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/310,802
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,795
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/361,159
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/373,050
; PRIOR FILING DATE: 2002-04-16

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; PRIOR APPLICATION NUMBER: 60/380,970
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/381,030
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/323,944
; PRIOR FILING DATE: 2001-09-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 41
; LENGTH: 709
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(709)
US-10-211-689-41

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Score: 92.00 Matches: 18
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DB: 7 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-211-689-41 (1-709)

Qy 1 MetLysValLeuTrpAlaLaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 14 ATGAAGGTTCTGTGGGCTGCTGTGTCACATTCTGCGAGGATGCCAGGCC 67

Search completed: June 15, 2006, 00:44:20
Job time : 130.918 secs

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 14, 2006, 22:11:12 ; Search time 3.12303 Seconds

(without alignments)
2035.043 Million cell updates/sec

Title: US-09-827-854A-13

Perfect score: 92

Sequence: 1 MKVLWAAALLVFLAGCOA 18

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 290227 seqs, 117694381 residues

Total number of hits satisfying chosen parameters: 580454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MTN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs04
-USER=US09827854 @CGN 1_139 @runat_14062006_081840_27029 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	75	81.5	5515	6	US-10-524-021-1 Sequence 1, Appli
2	50	54.3	3440	6	US-10-449-902-18081 Sequence 18081, A
3	48	52.2	1503	6	US-10-953-349-22323 Sequence 22323, A
4	48	52.2	118899	7	US-11-189-279-64 Sequence 64, Appl
5	47	51.1	2553	6	US-10-449-902-17095 Sequence 17095, A
6	45	48.9	151830	6	US-10-519-335-37 Sequence 37, Appl
7	44	47.8	586	6	US-10-449-902-28363 Sequence 28363, A
8	44	47.8	1371	6	US-10-449-902-10702 Sequence 10702, A
9	44	47.8	1425	6	US-10-449-902-1107 Sequence 1107, Ap

10	44	47.8	2618	6	US-10-449-902-25053 Sequence 25053, A
11	44	47.8	2794	6	US-10-449-902-13084 Sequence 13084, A
12	44	47.8	2892	6	US-10-449-902-27239 Sequence 27239, A
13	43.5	47.3	2260	6	US-10-449-902-21037 Sequence 21037, A
14	43.5	47.3	2265	6	US-10-449-902-15333 Sequence 15333, A
15	43.5	47.3	2392	6	US-10-449-902-24008 Sequence 24008, A
16	43	46.7	957	6	US-10-471-571A-2653 Sequence 2653, Ap
17	43	46.7	1063	6	US-10-449-902-12153 Sequence 12153, A
18	43	46.7	1146	7	US-11-217-529-2240 Sequence 2240, Ap
19	43	46.7	2353	6	US-10-449-902-26166 Sequence 26166, A
20	42	45.7	856	6	US-10-449-902-490 Sequence 490, App
21	42	45.7	1842	6	US-10-449-902-18852 Sequence 18852, A
22	42	45.7	1954	6	US-10-449-902-27158 Sequence 27158, A
23	42	45.7	2187	6	US-10-449-902-21820 Sequence 21820, A
24	42	45.7	2249	7	US-11-293-697-442 Sequence 442, App
25	42	45.7	2930	7	US-11-145-307A-1 Sequence 1, Appli
26	42	45.7	2934	7	US-11-217-529-79433 Sequence 79433, A
27	42	45.7	3486	6	US-10-449-902-12686 Sequence 12686, A
28	42	45.7	4282	6	US-10-449-902-18815 Sequence 18815, A
29	41.5	45.1	1477	6	US-10-953-349-13080 Sequence 13080, A
30	41.5	45.1	1486	6	US-10-953-349-22075 Sequence 22075, A
31	41.5	45.1	1842	6	US-10-449-902-7083 Sequence 7083, Ap
32	41.5	45.1	2484	6	US-10-449-902-14774 Sequence 14774, A
33	41.5	45.1	17402	7	US-11-296-119-8 Sequence 8, Appli
34	41	44.6	365	6	US-10-473-173-297 Sequence 297, App
35	41	44.6	381	7	US-11-217-529-166913 Sequence 166913, A
36	41	44.6	489	7	US-11-217-529-80129 Sequence 80129, A
37	41	44.6	510	6	US-10-488-619-2087 Sequence 2087, Ap
38	41	44.6	1391	6	US-10-449-902-8455 Sequence 8455, Ap
39	41	44.6	1481	6	US-10-449-902-18066 Sequence 18066, A
40	41	44.6	1635	6	US-10-953-349-36046 Sequence 36046, A
41	41	44.6	1654	6	US-10-449-902-20458 Sequence 20458, A
42	41	44.6	2307	7	US-11-293-697-1429 Sequence 1429, Ap
43	41	44.6	2891	6	US-10-449-902-24160 Sequence 24160, A
44	41	44.6	3072	7	US-11-293-697-1127 Sequence 1127, Ap
45	40	43.5	640	6	US-10-449-902-17714 Sequence 17714, A

ALIGNMENTS

RESULT 1
US-10-524-021-1
; Sequence 1, Application US/10524021
; Publication No. US200609590A1
; GENERAL INFORMATION:
; APPLICANT: NAGOYA INDUSTRIAL SCIENCE RESEARCH INSTITUTE
; APPLICANT: GIFU INTERNATIONAL INSTITUTE OF BIOTECHNOLOGY
; APPLICANT: YAMADA, Yoshihiro
; APPLICANT: YOKOTA, Mitsuhiko
; TITLE OF INVENTION: Method for diagnosing a risk of restenosis after percutaneous
; TITLE OF INVENTION: intervention
; FILE REFERENCE: C0200501
; CURRENT APPLICATION NUMBER: US/10/524, 021
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: JP P2002-233041
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5515
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-524-021-1

Alignment Scores:
Pred. No.: 0.00103 Length: 5515
Score: 75.00 Matches: 16
Percent Similarity: 88.9% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 2
Query Match: 81.5% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-524-021-1 (1-5515)

QY 1 MetLysValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 1871 ATGAAGTTCTGGGGCTGGTTGCTGGTACATTCTTGGCAGGTATGGGGCG 1924

RESULT 2

US-10-449-902-18081
; Sequence 18081, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18081
; LENGTH: 3440
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK068492
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-18081

Alignment Scores:
Pred. No.: 16.8 Length: 3440
Score: 50.00 Matches: 9
Percent Similarity: 71.4% Conservative: 1
Best Local Similarity: 64.3% Mismatches: 4
Query Match: 54.3% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-449-902-18081 (1-3440)

QY 3 ValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCys 16
Db 458 GTTCTGGGGTGGTTGTTGTTACTATGTTTTTTTGGTTCAATGT 499

RESULT 3

US-10-953-349-22323
; Sequence 22323, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCES-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22323
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22323

Alignment Scores:
Pred. No.: 13.7 Length: 1503
Score: 48.00 Matches: 8
Percent Similarity: 66.7% Conservative: 4
Best Local Similarity: 44.4% Mismatches: 6
Query Match: 52.2% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-953-349-22323 (1-1503)
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Db 1051 ATGGGATATTGGGCCCCCTCTGCCTCACTACGTTCCCGGTGCAACTCT 1104

RESULT 4

US-11-189-279-64
; Sequence 64, Application US/11189279
; Publication No. US20060115829A1
; GENERAL INFORMATION:
; APPLICANT: MAO, LI
; APPLICANT: WANG, JIE
; APPLICANT: LUO, WANG
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: UTXC-875US
; CURRENT APPLICATION NUMBER: US/11/189,279
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: 60/598,554
; PRIOR FILING DATE: 2004-08-03
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 118899
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-189-279-64

Alignment Scores:
Pred. No.: 3.17e-03 Length: 118899
Score: 48.00 Matches: 7
Percent Similarity: 80.0% Conservative: 5
Best Local Similarity: 46.7% Mismatches: 3
Query Match: 52.2% Indels: 0
DB: 7 Gaps: 0

US-09-827-854A-13 (1-18) x US-11-189-279-64 (1-118899)

QY 3 ValLeuTrpAlaAlaLeuValThrPheLeuAlaGlyCysGln 17
Db 57048 CTTCCTGGTCTCCGATTTCACGTGTTCTCTCTGGTCCAG 57092

RESULT 5

US-10-449-902-17095
; Sequence 17095, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17095
; LENGTH: 2553
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK067558
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-17095

Alignment Scores:
Pred. No.: 39.9 Length: 2553

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Score: 47.00 Matches: 8
Percent Similarity: 66.7% Conservative: 4
Best Local Similarity: 44.4% Mismatches: 6
Query Match: 51.1% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-449-902-17095 (1-2553)

Qy 1 MetLysValLeuTcAlaAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 1105 ATGTCATTGATGATGGCTTGGTGTAAACATACCTCACCGGTGCAGGTGCT 1158

RESULT 6
US-10-519-335-37/c
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
; APPLICANT: Cavarec, Laurent
; APPLICANT: Chumakov, Ilya
; APPLICANT: Destenaves, Benoit
; APPLICANT: Gonthier, Catherine
; APPLICANT: Elias, Isabelle
; TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN TH
; FILE REFERENCE: G-194US03PCT
; CURRENT APPLICATION NUMBER: US/10/519,335
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 60/391,359
; PRIOR FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 47
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; SEQ ID NO 37
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; ORGANISM: Homo sapiens
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; LOCATION: (143629)..(143629)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (149079)..(149079)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5363)..(5363)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8080)..(8080)
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OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (10296)..(10296)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14528)..(14528)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15336)..(15336)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15457)..(15457)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16288)..(16288)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16306)..(16307)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16316)..(16316)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16397)..(16397)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (56012)..(56012)
OTHER INFORMATION: n = a or c or g or t
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (1)..(54)
OTHER INFORMATION: exon 1
FEATURE:
NAME/KEY: exon
LOCATION: (55)..(124)
OTHER INFORMATION: exon 1
FEATURE:
NAME/KEY: exon
LOCATION: (91147)..(91244)
OTHER INFORMATION: exon 2
FEATURE:
NAME/KEY: exon
LOCATION: (93669)..(93834)
OTHER INFORMATION: exon 3
FEATURE:
NAME/KEY: exon
LOCATION: (96310)..(96422)
OTHER INFORMATION: exon 4
FEATURE:
NAME/KEY: exon
LOCATION: (99546)..(99723)
OTHER INFORMATION: exon 5
FEATURE:
NAME/KEY: exon
LOCATION: (125441)..(125605)

Alignment Scores:
Pred. No.: 151830
Score: 1.46e+04
Percent Similarity: 45.00
Length: 76.5%
Matches: 9
Conservative: 4

Best Local Similarity: 52.9% Mismatches: 4
Query Match: 48.9% Indels: 0
DB: 6 Gaps: 0
US-09-827-854A-13 (1-18) x US-10-519-335-37 (1-151830)
Qy 2 LysValLeuTrpAlaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 151567 AGGTTGTTGGTGGCGGATGGAATGATGTTCTCAGCCGGGTGCCAGGCC 151517
RESULT 7
US-10-449-902-28383/c
Sequence 28383, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28383
LENGTH: 586
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK103925
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-28383
Alignment Scores:
Pred. No.: 21.9 Length: 586
Score: 44.00 Matches: 7
Percent Similarity: 71.4% Conservative: 3
Best Local Similarity: 50.0% Mismatches: 4
Query Match: 47.8% Indels: 0
DB: 6 Gaps: 0
US-09-827-854A-13 (1-18) x US-10-449-902-28383 (1-586)
Qy 3 ValLeuTrpAlaLeuLeuValThrPheLeuAlaGlyCys 16
Db 346 GTCATGTGGAGCGCGTCCAGTTGACGTACTTGGCGGCTGC 305
RESULT 8
US-10-449-902-10702
Sequence 10702, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10702
LENGTH: 1371

; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK108050
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-110702

Alignment Scores:
Pred. No.: 63.3 Length: 1371
Score: 44.00 Matches: 7
Percent Similarity: 71.4% Conservatives: 3
Best Local Similarity: 50.0% Mismatches: 4
Query Match: 47.8% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-449-902-110702 (1-1371)

Qy 3 ValLeuTrpAlaLaLeuLeuValThrPheLeuAlaGlyCys 16
Db 787 GTCATGTGGAGCGCGTCCAGTTGACGTACTTGGCCGGCTGC 828

RESULT 9

US-10-449-902-1107/c
; Sequence 1107, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1107
; LENGTH: 1425

; TYPE: DNA
; ORGANISM: Oryza sativa

; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK059168

; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-1107

Alignment Scores:
Pred. No.: 66.4 Length: 1425
Score: 44.00 Matches: 7
Percent Similarity: 71.4% Conservatives: 3
Best Local Similarity: 50.0% Mismatches: 4
Query Match: 47.8% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-449-902-1107 (1-1425)

Qy 3 ValLeuTrpAlaLaLeuLeuValThrPheLeuAlaGlyCys 16
Db 1054 GTCATGTGGAGCGCGTCCAGTTGACGTACTTGGCCGGCTGC 1013

RESULT 10

US-10-449-902-25053
; Sequence 25053, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25053
; LENGTH: 2618
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK100495
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-25053

Alignment Scores:
Pred. No.: 142 Length: 2618
Score: 44.00 Matches: 8
Percent Similarity: 81.8% Conservatives: 1
Best Local Similarity: 72.7% Mismatches: 2
Query Match: 47.8% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-449-902-25053 (1-2618)

Qy 5 TrpAlaLaLeuLeuValThrPheLeuAlaGly 15
Db 2056 TGGCGCGGCTTCTGTGACCCCTAATCGCGGA 2088

RESULT 11

US-10-449-902-13084/c
; Sequence 13084, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13084
; LENGTH: 2794

; TYPE: DNA
; ORGANISM: Oryza sativa

; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK110432

; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-13084

Alignment Scores:
Pred. No.: 154 Length: 2794
Score: 44.00 Matches: 10
Percent Similarity: 76.5% Conservatives: 3
Best Local Similarity: 58.8% Mismatches: 4
Query Match: 47.8% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-449-902-13084 (1-2794)

Qy 2 LysValLeuTrpAlaLaLeuLeuValThrPheLeuAlaGlyCysGlnAla 18
Db 1516 CAGCTGCTGTCGGCGGCTGCTGCCCTCCAGCTGCGCAGCTGTACGCC 1466

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RESULT 12
US-10-449-902-27239
; Sequence 27239, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27239
; LENGTH: 2892
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: AK102681
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-27239
Alignment Scores:
Pred. No.: 160 Length: 2892
Score: 44.00 Matches: 7
Percent Similarity: 75.0% Conservative: 2
Best Local Similarity: 58.3% Mismatches: 3
Query Match: 47.8% Indels: 0
DB: 6 Gaps: 0

US-09-827-854A-13 (1-18) x US-10-449-902-27239 (1-2892)
Qy 5 TtpAlaAlaLeuValThrPheLeuAlaGlyCys 16
Db 1532 TGGGGCCATGATGGCCAGACCTTCCTATCGGGAIC 1567

RESULT 13
US-10-449-902-21037
; Sequence 21037, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21037
; LENGTH: 2260
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: AK071336
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-21037
Alignment Scores:
Pred. No.: 145 Length: 2260
```

```
Score: 43.50 Matches: 9
Percent Similarity: 73.7% Conservative: 5
Best Local Similarity: 47.4% Mismatches: 4
Query Match: 47.3% Indels: 1
DB: 6 Gaps: 1

US-09-827-854A-13 (1-18) x US-10-449-902-21037 (1-2260)
Qy 1 MetLysValLeuTrpAlaAlaLeu---LeuValThrPheLeuAlaGlyCysGlnAla 18
Db 1341 ATGGAAACCTTGCGCAGTTGGTAGTTGATATCCTTCTAAGTCCCTGTCAAGCA 1397

RESULT 14
US-10-449-902-15333
; Sequence 15333, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15333
; LENGTH: 2265
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: AK065861
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-15333
Alignment Scores:
Pred. No.: 145 Length: 2265
Score: 43.50 Matches: 9
Percent Similarity: 73.7% Conservative: 5
Best Local Similarity: 47.4% Mismatches: 4
Query Match: 47.3% Indels: 1
DB: 6 Gaps: 1

US-09-827-854A-13 (1-18) x US-10-449-902-15333 (1-2265)
Qy 1 MetLysValLeuTrpAlaAlaLeu---LeuValThrPheLeuAlaGlyCysGlnAla 18
Db 1401 ATGGAAACCTTGCGCAGTTGGTAGTTGATATCCTTCTAAGTCCCTGTCAAGCA 1457

RESULT 15
US-10-449-902-24008
; Sequence 24008, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
```



```
; SEQ ID NO 24008
; LENGTH: 2392
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1106)..(1106)
; OTHER INFORMATION: "n"=any one base of a, t, c, or g
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK099450
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-24008
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```
Alignment Scores:
Pred. No.:      156      Length:      2392
Score:          43.50     Matches:      9
Percent Similarity: 73.7%  Conservative: 5
Best Local Similarity: 47.4% Mismatches:      4
Query Match:      47.3%   Indels:      1
DB:               6      Gaps:      1
```

US-09-827-854a-13 (1-18) x US-10-449-902-24008 (1-2392)

```
Qy      1  MetLysValLeuTrpAlaAlaLeu---LeuValThrPheLeuAlaGlyCysGlnAla 18
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db      1369  ATGGAACAACTTGTGGCAGTTGGTGTAGTTGATATCCTTCCTAAGTGCTGCTCAAGCA 1425
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Search completed: June 14, 2006, 22:15:10
Job time : 9.12303 secs

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